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Search time 54.5455 Seconds (without alignments) 125.735 Million cell updates/sec

Aee88000 Human proAbp6585 Horse IgE
Abb64299 Drosophil
Ady24243 Pseudomon
Abm85909 Rice abio
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Act33307 Acinetoba
Aabol844 Haemophil
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Adq4996 SnSAG3 an
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Aag46697 Arabidops

AED15438 AEE88000 ABP64299 AD709532 AD709532 AD709532 ABM85909 AEE74334 AAB01845 AAB01845 AAB01845 AAB01845 AAG16359 AAG16359 AAG16399 AAG16396 AAG16396 AAG16396 AAG16396 AAG16396 AAG16396 AAG16396 AAG16396

US-10-758-165A-1 81

1 RNDSPIQTDQYTTTG 15 Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2589679 segs, 457216429 residues Searched: Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 sed Minimum DB Maximum DB Minimum Match 0% Maximum Match 100% Listing first 45 summaries Post-processing:

ALIGNMENTS

Geneseq_8:* Database

Genesequ1980s;
genesequ1990s;
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genesequ2001s;
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genesequ2001s;
genesequ2005s;
genesequ2005s;

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Adr10601 Dog IgE e		_	Aar97753 Canine Ig			Pig	Cat	Adg73237 Cat immun	Cat		Abu09336 Feline Ig	_	Adg73225 Cat parti	Abu42513 Protein e	Abb91309 Herbicida	Adr10603 Horse IgE	Aau57418 Propionib	Abm53937 Propionib	. Aam50103 Equine Ig			Ads05754 Staphyloc
ΙD	ADR10601	AAY79995	AAW23067	AAR97753	ABP96583	ADR10607	ABP96588	ADR10602	ADG73237	ABP96580	ABU09338	ABU09336	ADG73251	ADG73225	ABU42513	ABB91309	ADR10603	AAU57418	ABM53937	AAM50103	AAM50104	ABP39208	ADS05754
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Length	15	312	417	426	426	15	567	15	431	496	496	496	496	496	1633	1067	15	151	151	424	424	533	533
Query	100.0	100.0	100.0	100.0	100.0	65.4	65.4	59.3	59.3	59.3	59.3	59.3	59.3	59.3	53.1	51.9	50.6		50.6		50.6	50.6	50.6
Score	81	81	81	81	81	53	23	48	48	48	48	48	48	48	43	42	41	41	41	41	41	41	41
Result No.	1	7	m	4	5	9	7	80	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23

CCCCCCCXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	ADRIO601 standard; peptide; 15 AA. ADRIO601; 21-OCT-2004 (first entry) Dog IgE epitope recognised by monoclonal antibody 5. Antiasthmatic; Antiallergic; Immunosuppressive; IgE; anaphylactic shock; 5.91 monoclonal antibody; 3.76 m Canis familiaris. WO2004065936-A2. 05-AUG-2004. 15-JAN-2003; 2003US-0440472P. (UTNC-) UNIV NORTH CAROLINA STATE. Hammerberg B; WPI; 2004-593545/57. Novel antibody that specifically binds to mammalian for testing an allergen reactivity of IgE sample, de or treating asthma or anaphylactic shock. Example 6; Page 9; 14pp; English. The present invention relates to a novel monoclonal specifically binds to mammalian IgE epitope, where between amino acids 145-166 or 356-374 of mammalian (I) is useful for testing an allergen reactivity of and corn allergens. The sample is a biological sample dog, cat or horse. (I) is also useful for detecting and corn allergens. The sample is a biological sample dog, cat or horse. (I) is also useful for detecting
8888	treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclon antibodies recognise epitopes on canine IgE corresponding to amin residues 357-371 (ADR10601) and 146-162 (ADR10609) respectively or the state of t
ပ္ပ	canine IgE epsilon-chain. Recognition of epsilon-chains from IgE from

100.08;

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Best Local Similarity
Matches 15, Conserv
                                                                                                                                                                                                                                                                              RESULT 3
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cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and 3.76 ware observed to have good cross-reactivity with the epsilon-chain of IgE from cat and horse, but did not exhibit cross-reactivity with either pig or human epsilon-chains of IgE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen; immunoglobulin limmunostimulatory; carrier protein; helper T cell epitope; antibody; allergy; allergy; disease; immunisation; anti-allergic; anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.
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                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                              100.0%; Score 81; DB 8; Length 15; 100.0%; Pred. No. 5.9e-07;
                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                  Mismatches
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                                                                                                                                                                                  Sequence 15 AA;
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Length 312;

DB 3;

100.0%; Score 81;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This polypeptide is encoded by exons 1-4 (see AAT79278) of canine IgE heavy chain constant region (epsilon) genomic DNA. Another polypeptide, comprising the exon 5 and 6 product, is given in AAW23068. Recombinant peptides encoded by exons 1-6 can be produced in eukaryotic or prokaryotic cells. Such peptides, and antibodies raised against them, a used in methods to treat the manifestation of allersy in dogs, e.g. to treat Type I immediate hypersensitivity, and for immunomodulation
              Gaps
                                                                                                                                                                                                                                                  IgE; immunoglobulin; antibody; heavy chain constant region; allergy; hypersensitivity; therapy; dog; antisense; immunomodulation.
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0
                                                                                                                                                                                                                            Canine IgE heavy chain constant region (exon 1-4 product).
            Indels
Pred. No. 1.5e-05;
Mismatches 0;
              Mismatches
                                                                                                                                                                                                                                                                                                                                                                 'note= "encoded by TAC"
                                                                                                                                                                                                                                                                                                                                                                                         'note= "encoded by GCC"
                                                                                                                                                                                                                                                                                                                                                                                                                 by NNT"
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Misc-difference 55
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                                                      255 RNDSPIQTDQYTTTG 269
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                                      1 RNDSPIQTDQYTTTG
               Conservative
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N-PSDB; AAT79278.
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                                                                                                                                                                            30-JUN-2005
16-JUN-2005
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Matches

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RESULT 4

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Identifying peptides that induce cytotoxic T-lymphocyte, CTL response against IgE, by identifying peptide eliciting CTL response to IgE peptides naturally presented by major histocompatibility complex class I
                                                                                                                                    antiallergic; antiaethmatic; immunosuppressivė; vasotropic; cytostatic; dermatological; antinflammatory; igg-mediated condition; food allergy; atopic hypersensitivity condition; allergic rhinitis; allergic asthma; atopic dermatitis; non-atopic hypersensitivity condition; anaphylaxis;
                                                                                                      Immunoglobulin E, vaccine, IgE, cytotoxic T lymphocyte response; immune response; major histocompatibility complex; MHC; immunoge
                                                                         Dog IgE heavy chain amino acid sequence SEQ ID NO:28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 7; Page 152-154; 187pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                         Yang Y, Barankiewicz T,
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                                                                                                                                                                                                                                                                                                                                                           13-AUG-2001; 2001US-0312120P.
                                                                                                                                                                                                                                                                                                                                                                                          (IGET-) IGE THERAPEUTICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 RNDSPIQTDQYTTTG 15
                                            28-MAY-2003 (first entry)
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Best Local Similarity
Matches 15; Conserv
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                                                                                                                                                                                                     urticaria hives.
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                                                                                                                                                                                                                                                                                               27-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     can be used in drug development (e.g. small molecule screening, assay development and anti-1gE antibody generation). Fragments of 1gE can be used in vaccines or to prevent 1gE-mediated hypersensitivity. The new sequence information permits targeted modulation of 1gE-mediated immune
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                                                                                                        Gaps
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Pred. No. 2.1e-05;
Mismatches 0; Indels
                                                                         Length 417;
                                                                                                      0; Indels
             Revised record issued on 30-JUN-2005 : Typo in comments
                                                                       100.0%; Score 81; DB 2; I 100.0%; Pred. No. 2.1e-05;
                                                                                                        Mismatches
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100.0%;
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                                                                                                                                     1 RNDSPIQTDQYTTTG 15
                                                                                                                                                                                                                                                                                                            (first entry)
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nes 15; Conservative
                                                                                                        15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hollis GF, Patel MD;
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                                                                                        Local Similarity
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                                                                         Query Match
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The present invention describes a method (M1) for identifying peptides that induce cytotoxic T-lymphocyte (CTL) response against immunoglobulin E [IgB], comprising providing a test peptide (T) suspected of being able to bind to major histocompatibility complex (WHC) class I molecule, and evaluating (T) for ability to elicit in a mammal a CTL response to naturally processed and presented IgE peptides, where a peptide that induces such a response is identified. Also described are compositions: (C1) comprising at least one immunogenic peptide (I) identified by (M1); (C2) comprising at least one isolated polymicleotide encoding (I); and (C3) comprising antiqen-presenting cells that recognise at least one (I). Where C1-3 are able to bind to at least one MHC class I molecule and to elicit in a mammal a CTL response to naturally processed and presented IgE peptides. C1-3 have antiallargic, antiasthmatic, immunosuppressive, vasotropic, dermatological, antiallargic, antiasthmatic, immunosuppressive, vaccines. C1-3 can be used for modulating an IgE-mediated condition in a mammal. C1-3 are useful for modulating an IgE-mediated condition such as IgE-mediated anti-proposition of the condition, IgE-mediated non-atopic of the condition of the condition in the condition of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypersensitivity condition, IgE myeloma in a mammal. Preferably, Cl-3 are useful for treating atopic hypersensitivity conditions (such as allergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       atopic hypersensitivity conditions (such as anaphylaxis, and urticaria hives). The present sequence represent on Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Pred. No. 2.1e-05;
Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                357 RNDSPIQTDQYTTTG 371
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ABP96583 standard; protein; 426 AA.

RESULT 5 ABP96583 ID ABP9

Matches

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Identifying peptides that induce cytotoxic T-lymphocyte, CTL response against IgE, by identifying peptide eliciting CTL response to IgE peptides naturally presented by major histocompatibility complex class I
                                                                immune response; major histocompatibility complex; MHC; immunogenic; antiallergic; antiasthmatic; immunosuppressive; vasotropic; cytostatic; dermatoly; igg-mediated condition; food allergy; apprepation; production; food allergy; apprepation; hypersensitivity condition; allergic rhinitis; allergic asthma; atopic dermatitis; non-atopic hypersensitivity condition; anaphylaxis;
                                             Immunoglobulin E; vaccine; IgE; cytotoxic T lymphocyte response;
Pig IgE heavy chain amino acid sequence SEQ ID NO:33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 7; Page 164-167; 187pp; English.
                                                                                                                                                                                                                                                                                                                                                        08-AUG-2002; 2002WO-US026986.
                                                                                                                                                                                                                                                                                                                                                                                                   13-AUG-2001; 2001US-0312120P.
                                                                                                                                                                                                                                                                                                                                                                                                                                               (IGET-) IGE THERAPEUTICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-268242/26.
                                                                                                                                                                              urticaria hives.
                                                                                                                                                                                                                                                                   WO2003015716-A2
                                                                                                                                                                                                                                                                                                                 27-FEB-2003
                                                                                                                                                                                                                            Sus scrofa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chen SA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein.
      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to a novel monoclonal antibody (I) that specifically binds to a mammalian IgE epitope, where the epitope is between amino acids 145-146 or 356-374 of mammalian IgE, e.g. dog IgE. (I) is useful for testing an allergen reactivity of an IgE sample. The allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut and corn allergens. The sample is a biological sample collected from a dog, cat or horse. (I) is also useful for detecting mammalian IgE and for treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal antibodies recognise epitopes on canine IgE corresponding to amino acid residues 357-371 (ADRIGOGI) and 146-162 (ADRIGOGO) respectively of the canine IgE epsilon-chain. Recognition of epsilon-chains from IgE from cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel antibody that specifically binds to mammalian IgE epitope, useful for testing an allergen reactivity of IgE sample, detecting mammalian IgE or treating asthma or anaphylactic shock.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.76 were observed to have good cross-reactivity with the epsilon-chain of IgE from cat and horse, but did not exhibit cross-reactivity with either pig or human epsilon-chains of IgE. The present sequence is the pig IgE 5.91 recognition site.
                                                                                                                                                                                                                                                Antiasthmatic; Antiallergic; Immunosuppressive; IgE; dog; asthma; anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                  Pig IgE epitope recognised by monoclonal antibody 5.91, SEQ ID 7.
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Pred. No. 0.044;
5; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYNC-) UNIV NORTH CAROLINA STATE.
                                                                       ADR10607 standard; peptide; 15 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 6; Page 9; 14pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JAN-2004; 2004WO-US003566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-JAN-2003; 2003US-0440472P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 RNDSPIQTDQYTTT 14
                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2004-593545/57.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                 WO2004065936-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hammerberg B;
                                                                                                                                                           21-OCT-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cat, horše,
3.76 were ob
                                                                                                                                                                                                                                                                                                                                                                                                                            05-AUG-2004
                                                                                                                                                                                                                                                                                                                                        Sus scrofa.
                                                                                                                  ADR10607;
                                                  ADR10607
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2 Chen

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Yang Y, Barankiewicz

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The present invention describes a method (M1) for identifying peptides that induce cytotoxic T-lymphocyte (CTL) response against immunoglobulin (CC that induce cytotoxic T-lymphocyte (CTL) response against immunoglobulin (CC to bind to major histocompatibility complex (MHC) class I molecule, and evaluating (T) for ability to elicit in a mammal a CTL response to induces such a response is identified. Also described are compositions: (CC) comprising at least one immunogenic peptide (I) identified by (M1); (C2) comprising at least one immunogenic peptide (I) identified by (M1); (C2) comprising at least one isolated polynucleotide encoding (I); and (CC) comprising at least one isolated polynucleotide encoding (I); and (CC) comprising at least one isolated polynucleotide encoding (I); and (CC) comprising at least one isolated polynucleotide encoding (I); and (CC) comprising at least one isolated polynucleotide encoding (I); and (CC) comprising at least one isolated polynucleotide encoding (I); and (CC) comprising at least one isolated polynucleotide encodic (I) and (CC) comprising at least one isolated polynucleotide encodic (I); and (CC) comprising at least one isolated polynucleotide encodic (I); and (CC) comprising an inducers of actIL response against IgE, and in command (I) are useful for modulating an IgE-mediated condition in a compositivity condition, IgE myeloma in a mammal. Preferably, CI-3 are useful for treating atopic hypersensitivity condition; IgE-mediated one-atopic characting atopic hypersensitivity conditions (such as anaphylaxis, and urticaria atopic hypersensitivity conditions (such as anaphylaxis, and urticaria conditions). The present sequence represents an IgE-mediated acopic hypersensitivity conditions (such as anaphylaxis, and urticaria conditions). In this is allergic asthma, food allergies, or atopic dermaticaria.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hives). The present sequence represents an IgE heavy chain amino acid sequence, which is given in an example from the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 567;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 53; DB 6;
Pred. No. 2.2;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADR10602 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65.4%;
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RNDAPVQADRHSTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RNDSPIOTDOYTTT
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es 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 567 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    499
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ID ADR1
XX
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ABP96588 standard; protein; 567 AA.

RESULT 7 ABP96588 (first entry)

28-MAY-2003

ABP96588;

8 g

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The invention describes an isolated nucleic acid molecule (I) encoding a portion of a feline IgE heavy chain protein. The methods and compositions of the present invention are useful for eliciting feline immune responses for and/or treating IGE-mediated responses, such as allergies. This is the amino acid sequence of a cat immunoglobulin E (IgE) constant region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunoglobulin E, vaccine, IgE, cytotoxic T lymphocyte response; immune response; major histocompatibility complex; MHC; immunogenic; antiallergic; antiaethmatic; immunosuppressive; vasotropic; cytostatic; dermatological; antiinflammatory; IgE-mediated condition; food allergy; atopic hypersensitivity condition; allergic rhinitis; allergic asthma; atopic dermatitis; non-atopic hypersensitivity condition; anaphylaxis;
                                                                                                                                                                                                                                                                                                                                                                                                     New isolated nucleic acid molecule encoding a portion of a feline igB heavy chain protein, useful for treating and/or eliciting feline immur responses for IGE-mediated responses, such as allergies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cat IgE heavy chain amino acid sequence SEQ ID NO:25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 48; DB 8;
Pred. No. 12;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chen Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 12; SEQ ID NO 14; 44pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABP96580 standard; protein; 496 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yang Y, Barankiewicz T,
                                                                                                                          07-APR-2003; 2003US-00409772.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-AUG-2002; 2002WO-US026986.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-AUG-2001; 2001US-0312120P.
                                                                                                                                                                  07-JAN-1999; 99US-0115033P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (IGET-) IGE THERAPEUTICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ||||::|:|
|NDSPVRTEQQATT 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-MAY-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 NDSPIQTDQYTTT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8; Conservative
                                                                                                                                                                                                                                                                                                                                         WPI; 2004-010802/01
                                                                                                                                                                                                                                                                                                 C, Weber E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                MCCALL C. WEBER E.
                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; ADG73236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 431 AA;
                                        US2003216565-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      urticaria hives.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO2003015716-A2
Felis catus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Felis catus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-FEB-2003
                                                                                20-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          363
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                                                                                                                                                                                                                                (MCCA/)
(WEBE/)
                                                                                                                                                                                                                                                                                                 Mccall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABP96580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to a novel monoclonal antibody (I) that specifically binds to a mammalian IgE epitope, where the epitope is between amino acids 145-166 or 356-374 of mammalian IgE, e.g. dog IgE. (I) is useful for testing an allergen reactivity of an IgE sample. The allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut and corn allergens. The sample is a biological sample collected from a dog, cat or horse. (I) is also useful for detecting mammalian IgE and for treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel antibody that specifically binds to mammalian IgE epitope, useful for testing an allergen reactivity of IgE sample, detecting mammalian IgE or treating asthma or anaphylactic shock.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antibodies recognise epitopes on canine IgE corresponding to amino acid residues 357-371 (ADR10601) and 146-162 (ADR10609) respectively of the canine IgE epsilon-chain. Recognition of epsilon-chains from IgE from cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and 3.76 were observed to have good cross-reactivity with the epsilon-chain of IgE from cat and horse, but did not exhibit cross-reactivity with either pig or human epsilon-chains of IgE. The present sequence is the cat IgE 5.91 recognition site.
                                                                                                                        Antiasthmatic; Antiallergic; Immunosuppressive; IgE; dog; asthma; anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antiallergic, IgE-modulator, vaccine, feline, IgE; immunoglobulin E; immune response; IgE-mediated response; allergy; cat; constant region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                  Cat IgE epitope recognised by monoclonal antibody 5.91, SEQ ID 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 48; DB 8; Length 15; Pred. No. 0.33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cat immunoglobulin E (IgE) constant region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADG73237 standard; protein; 431 AA
                                                                                                                                                                                                                                                                                                                                                                                                                           (UYNC-) UNIV NORTH CAROLINA STATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 6; Page 9; 14pp; English.
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                                                                                                                                                                                                                                                                                                                                           15-JAN-2004; 2004WO-US003566.
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                                                                                                                                                                                                                                                                                                                                                                                   16-JAN-2003; 2003US-0440472P
                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ||||::|:|
2 NDSPVRTEQOATT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2004-593545/57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
8; Conserva
                                                                                                                                                                                                                                                       WO2004065936-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hammerberg B;
                                          21-OCT-2004
                                                                                                                                                                                                            Felis catus.
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Matches

RESULT 9 ADG7323

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Length 431; 2; Indels

eliciting feline immune

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                                                                                                                                                                                                                                                                                                                                         The present invention describes a method (M1) for identifying peptides that induce cytotoxic T-lymphocyte (CTL) response against immunoglobulin E [192], comprising providing a test peptide (T) suspected of being able to bind to major histocompatibility complex (MHC) class I molecule, and evaluating (T) for ability to elicit in a mammal a CTL response to naturally processed and presented IgS peptides, where a peptide that induces such a response is identified. Also described are compositions: (C1) comprising at least one immunogenic peptide (I) identified by (M1); (C2) comprising at least one immunogenic peptide (I) identified by (M1); (C3) comprising antigen-presenting cells that recognise at least one (I). Where C1-3 are able to bind to at least one MHC class I molecule and to elicit in a mammal a CTL response to naturally processed and presented ISE peptides. C1-3 have antiallergic, antiasthmatic, immunosuppressive, vasotropic, dermatological, antiinflammatory and cytostatic activities, and can be used as inducers of a CTL response against IgE, and in mammal. C1-3 are useful for modulating an IgE-mediated condition in a mammal. C1-3 are useful for modulating an IgE-mediated non-atopic to the constitution of the mammal of the mediated of the modulating an IgE-mediated non-atopic to the constitution of the mammal of the condition in a mammal. C1-3 are useful for modulating an IgE-mediated non-atopic to the constitution of the mammal of the condition in a mammal can be used as inducers of a CTL response against IgE-mediated non-atopic to the condition of the mammal can be used an object of the condition of the mammal can be used as inducers of a CTL response against IgE-mediated on-atopic to the condition of the mammal can be used as inducers of a CTL response against IgE-mediated non-atopic to the condition of the mammal can be used as inducers of a CTL response against IgE-mediated non-atopic condition.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypersensitivity condition, IgE myeloma in a mammal. Preferably, Cl-3 are useful for treating atopic hypersensitivity conditions (such as allergic rhinitis, allergic asthma, food allergies, or atopic dermatitis), nonatopic hypersensitivity conditions (such as anaphylaxis, and urticaria hives). The present sequence represents an IgE heavy chain amino acid sequence, which is given in an example from the present invention
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                                                                                                 Identifying peptides that induce cytotoxic T-lymphocyte, CTL response against IgE, by identifying peptide eliciting CTL response to IgE peptides naturally presented by major histocompatibility complex class
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Pred. No. 14;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                     Example 7; Page 145-147; 187pp; English
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                             WPI; 2003-268242/26.
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Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 496 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US2003013183-A1.
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                                                                           New nucleic acid molecule encoding feline immunoglobulin E (IgE) heavy or light chain protein, useful for treating feline IgE-mediated responses e.g. allergies, parasitic infections or neoplasia.
                                                                                                                                                                            The present invention relates to the isolation of feline immunoglobulin (IgB) kappa light chain and IgB epsilon heavy chain proteins, and the polynucleotide sequences encoding them. The sequences of the invention are useful for treating feline IgB-mediated immune responses (e.g. allergies, parasitic infections or neoplasia), in vaccine technology, small molecule/antibody technology, molecular biology, and various immunological techniques related to feline IgB and its functions. The present sequence represents feline IgB epsilon heavy chain #2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Feline, immunoglobulin B; IgE epsilon heavy chain; parasitic infection; IgE-mediated immune response; allergy; neoplasia; vaccine technology; antiallergic; antiparasitic; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "This sequence is given as SEQ ID No:14 and is specifically claimed in Claim 12" 284. .309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "This sequence is given as SEQ ID No:11 and is specifically claimed in Claim 9"
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                                                                                                                                                                                                                                                                                                                                                                Length 496;
                                                                                                                                                                                                                                                                                                                                                                                                2; Indels
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                                                                                                                                                                                                                                                                                                                                                                 Score 48;
Pred. No.
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                                                                                                                                                Claim 1; Page 37-39; 45pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Feline IgE epsilon heavy chain #1.
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specifically
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428 NDSPVRTEQQATT 440
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Weber E;
                                WPI; 2003-391997/37
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                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (WEBE/) WEBER E.
                                                  N-PSDB; ABX95715
                                                                                                                                                                                                                                                                                                                                  Sequence 496 AA;
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 Mccall C,
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Length 496;

DB 8;

Score 48; Pred. No.

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61.5%;
                                 Query Match
Best Local Similarity
Local 8; Conserv?
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                                                                                                                                                                                                                                                                                                                                                                                                                                          (MCCA/) MCCALL C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; ADG73224
                       Sequence 496 AA;
                                                                                                                                                                                                                                                                                                                                US2003216565-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      WEBER E.
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ID ABU4251
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chain.
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                                                                                                                                                     RESULT 14
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                                                                                                            The present invention relates to the isolation of feline immunoglobulin E (IgE) kappa light chain and IgE epsilon heavy chain proteins, and the polymucleotide sequences encoding them. The sequences of the invention are useful for treating feline IgE-mediated immune responses (e.g. allergies, parasitic infections or neoplasia), in vaccine technology, amall molecule/antibody, technology, molecular biology, and various immunological techniques related to feline IgE and its functions. The present sequence represents feline IgE epsilon heavy chain #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention describes an isolated nucleic acid molecule (I) encoding a portion of a feline IgE heavy chain protein. The methods and compositions of the present invention are useful for eliciting feline immune responses for and/or treating IGE-mediated responses, such as allergies. This is the amino acid sequence of a partial cat immunoglobulin E (IgE) heavy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated nucleic acid molecule encoding a portion of a feline IgE heavy chain protein, useful for treating and/or eliciting feline immune responses for IGE-mediated responses, such as allergies.
                                           New nucleic acid molecule encoding feline immunoglobulin E (IgE) heavy light chain protein, useful for treating feline IgE-mediated responses e.g. allergies, parasitic infections or neoplasia.
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                                                                                                                                                                                                                                               Score 48; DB 6; Length 496;
Pred. No. 14;
3; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 8; SEQ ID NO 29; 44pp; English.
                                                                                       Claim 1; Page 24-25; 45pp; English
                                                                                                                                                                                                                                                                                                                                                                               ADG73251 standard; protein; 496 AA
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61.5%;
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428 NDSPVRTEQQATT 440
                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                              NDSPIQTDQYTTT 14
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                                                                                                                                                                                                                                 Query Match
Best Local Similarity
8; Conserv?
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                     N-PSDB; ABX95713
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                                                                                                                                                                                                                        Sequence 496 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid molecule encoding a portion of a feline IgE heavy chain protein, useful for treating and/or eliciting feline immune responses for IGE-mediated responses, such as allergies.
  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antiallergic; IgE-modulator; vaccine; feline; IgE; immunoglobulin E; immune response; IgE-mediated response; allergy; cat; heavy chain.
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  2; Indels
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3; Mismatches
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3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABU42513 standard; protein; 1633 AA.
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                                                                                                                                                                                                                                                ADG73225 standard; protein; 496 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-APR-2003; 2003US-00409772.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-JAN-1999; 99US-0115033P.
07-JAN-2000; 2000US-00479614.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59.38;
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                                                                                                              428 NDSPVRTEQQATT 440
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  Conservative
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NDSPVRTEQOATT
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(first entry)

ABU42513;

Antisense; prokaryotic essential gene; cell proliferation; drug design. Protein encoded by Prokaryotic essential gene #28040. 21-MAR-2001; 2001US-00815242. 06-SEP-2001; 2001US-00948933. 25-OCT-2001; 2001US-0342923P. 08-FEB-2002; 2002US-00072861. 06-MAR-2002; 2002US-0362699P. 21-MAR-2002; 2002WO-US009107 Staphylococcus epidermidis (ELIT-) ELITRA PHARM INC. WO200277183-A2. 19-JUN-2003 03-OCT-2002. Wang L, Wall D,

WPI; 2003-029926/02.

Zyskind JW; Xu HH; Ohlsen KL, Forsyth RA, Haselbeck R, Yamamoto R, Malone C, Carr GJ, Zamudio C, Trawick JD,

N-PSDB; ACA46383

New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.

Claim 25; SEQ ID NO 70437; 1766pp; English.

the 6213 antisenes sequences given in the specification where expression of the 6213 antisenes esquences given in the specification where expression of the nucleic acid inhibits proliferation of a call. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation, or the activity of a gene in an operon required for proliferation or that has an activity against a biological pathway compared for proliferation or that has an activity against a biological pathway in which a proliferation or the test compound that inhibits spoilferation of an organism acts; (9) manufacturing an antibiotis; (10) profiling a gene required for required for collular proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound, sactivity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to by which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits profileration of an organism. The antisense mucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the sequences. The invention relates to an isolated nucleic acid comprising any one of

Sequence 1633 AA;

ö Gaps ; 0 h Similarity 61.5%; Pred. No. 3.7e+02; 8; Conservative 1; Mismatches 4. 7-2-7. Query Match Best Local Similarity Matches 8; Conserv

242 NDEPTODVEYTT 254 2 NDSPIQTDOYTTT 14 g ò

Search completed: August 30, 2006, 04:22:07 Job time : 55.5455 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

August 30, 2006, 04:29:42 ; Search time 8.93939 Seconds (without alignments)
161.448 Million cell updates/sec Run on:

US-10-758-165A-1 81 Perfect score:

1 RNDSPIQTDQYTTTG 15 Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		de			SUMMARIES	
Result No.	Score	Query Match	Length	88	ID	Description
	43	53.1	664	7	T20420	hypothetical prote
7	42	51.9	1008	N	T32986	
m	42	51.9	1067	~	D96545	probable DNA polym
4	41	50.6	1117	N	863399	
ß	40	49.4	234	~	T49737	hypothetical prote
9	40	49.4	1157	~	F97255	Q
7	40	6	2094	N	S33124	tpr protein - huma
œ	39	48.1	187	7	JC4806	core protein G - p
თ	39	48.1	187	~	S22331	gene G protein - p
10	39	48.1	294	7	T08408	transcription fact
11	39	48.1	514	N	S72443	DNA-binding protei
12	39	48.1	564	7	HMIVDA	hemagglutinin prec
-	39	48.1	587	7	F85084	probable athila-li
14	39	48.1	940	N	T01834	hypothetical prote
15	39	48.1	2161	Н	A45389	genome polyprotein
16	39	48.1	26926	-1	I38344	titin, cardiac mus
17	38.5	47.5	1157	Н	S49247	parasporal crystal
18	38	46.9	173	N	855150	аJ
19	38		201	N	T31492	
20	38	46.9	205	0	T31489	
21	38	46.9	254	~	F81265	cysQ protein homol
22	38		281	~	AD2052	hypothetical prote
23	38	٠	321	~	B32801	ď
24	38	٠	335	N	JE0115	zinc-finger protei
25	38	46.9	429	N	E84410	GTP-binding protei
56	38	•	450	N	A10345	probable heat shoc
27	38	46.9	468	0	T08139	shaggy-like protei
28	38	ė.	612	0	C90374	hypothetical prote
29	38	46.9	966	0	S76194	

hypothetical prote	165K myofibrillar	165K protein, skel	DNA-directed RNA p	hypothetical prote	glutamate racemase	hypothetical prote	extensin-like prot	probable cardiolip	agrocinopine utili	hypothetical prote					
AF1852	A44027	S43529	T07323	T38495	B69688	863193	F84234	B71841	T23844	A71966	A70238	T06296	E71963	A48650	AI3244
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1158	1450	1465	1562	1969	272	590	136	219	245	268	298	429	502	521	521
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46	46	46	46.9	46	46	46	45	45	45	45	45	45.7	45.7	45.7	45.7
38	38	38	38	38	37.5	37.5	37	37	37	3.7	37	37	37	37	37
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-664 <MIL>
A;Residues: 1-664 <MIL>
A;Cross-references: UNIPROT:Q19038; UNIPARC:UPI0000129186; EMBL:Z68003; PIDN:CAA91975.1;
A;Experimental source: clone E02H4
C;Genetics:
A;Gene: CESP:E02H4.1
                                                                                                                                                                                                                                                                                                                                                                                             A, Map position: X
A,Introns: 57/3; 102/3; 135/3; 166/1; 191/1; 221/2; 254/3; 314/2; 355/2; 386/1; 472/3; 5
C,Superfamily: human amiloride-sensitive sodium channel protein; fibronectin type I repe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
hypothetical protein E02H4.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T20420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53.1%; Score 43; DB 2; ilarity 80.0%; Pred. No. 16; Conservative 0; Mismatches
                                                                                                                 R;Barlow, K. submitted to the EMBL Data Library, November 1995 submitted number: Z19273 A;Reference number: Z19273 A;Accession: T20420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 536 PCQQDQYTTT 545
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les 8; Conserv
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Matches
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hypothetical protein C05D2.6 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999 C;Accession: T32986

R,Du, Z. submitted to the EMBL Data Library, February 1998 A;Description: The sequence of C. elegans cosmid C05D2 A;Reference number: Z21260

A;Accession: T32986
A;Status: preliminary: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Rostatiuss: 1-1008 < DUZ>
A;Cross-references: UNIPARC:UPI000017B734; EMBL:AF047651; PIDN:AAÇ02723.1; GSPDB:GN00021
A;Experimental source: strain Bristol N2; clone C05D2 C;Genetics:

A; Gene: CESP: C05D2.6

A;Map position: 3 A;Introns: 23/1; 53/3; 141/1; 231/3; 307/3; 325/2; 420/1; 466/3; 499/3; 522/2; 594/1; 75

51.9%; Score 42; Query Match

Length 1008;

DB 2;

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F97255 tutusion of alpha-glucosidase (family 31 glycosyl hydrolase) and glycosidase (TreA/MalS fautusion of alpha-glucosidase (TreA/MalS fautusion C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
B;Nolling, 0: Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, Jall, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
Barceriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clos A;Reference number: A96900; MUID:21359325; PMID:21359325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Homo sapiens (man)
C;Species: Alow-1993 #sequence revision 26-May-1995 #text_change 09-Jul-2004
C;Accession: 333124; S23740; $00928; $01185
C;Accession: 533124; S23740; $009er, C.S.
Oncogene 7, 2329-2333, 1992
Oncogene 7, 2329-2333, 1992
A;Title: The human tpr gene encodes a protein of 2094 amino acids that has extensive coi. A;Reference number: $33124; MUID:93064711; PMID:1437155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:097F62; UNIPARC:UPI00000D755C; GB:AE001437; PIDN:AAK80833.1;
A;Experimental source: Clostridium acetobutylicum ATCC824
                                                                                                                                                                                            A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: Lona
A;Molecule type: Lona
A;Molecule type: Lona
A;Cross-references: UNIPARC:UP10000179D8A; EMBL:AL356192; GSPDB:GN00116; NCSP:B24B19.90
A;Experimental source: BAC clone B24B19; strain OR74A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tpr protein - human
N,Alternate names: kinase-related transforming protein (tpr-met); protein with promoter
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                                                                                                                                                    C;Species: Neurospora crassa
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 18-Aug-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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C;Superfamily: Neurospora crassa hypothetical protein B24B19.90
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                                                                                                             - Neurospora crassa
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Pred. No. 17;
1; Mismatches
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Pred. No. 1e+02;
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                                                                                                         lypothetical protein B24B19.90 [imported]
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NESDVFTEQYTT 900
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Best Local Similarity
7; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene: NCSP: B24B19.90
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                                                                                                                                                                                                                                                                                                                                                                            A; Accession: T49737
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                                                                                                                                                                                                                                                                                                                                                            probable DNA polymerase A family protein [imported] - Arabidopsis thaliana probable DNA polymerase A family protein [imported] - Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar.2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: D96545
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunder, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lucos, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwisck, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.; M.; Venter, Off.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Accession: D96545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ď
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N;Alternate names: hypothetical protein N3547
C;Species: Saccharomyces cerevisiae
C;Date: 27-Apr-1996 #sequence_revision 03-May-1996 #text_change 09-Jul-2004
C;Accession: S63399
R;Duesterhoeft, A.; Floeth, M.; Fritz, C.; Heuss-Neitzel, D.; Hilbert, H.; Moestl, D. A;Reference number: S6294
A;Reference number: S6294
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-117 *DUBS
A;Cross-references: UNIPROT: P53753; UNIPARC:UPI000013BACB; EMBL:Z71682; NID:g1302597; B;A;Conse-references: Strain S288C
C;Genetics: MIPS:YNR057C
A;Genetics: MIPS:YNR057
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                   3; Indels
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A;Map position: 14R
C;Keywords: transmembrane protein
F;6-22/Domain: transmembrane #status predicted <TMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 42; DB 2
Pred. No. 41;
5; Mismatches
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58.3%; Pred. No. 39; ive 2; Mismatches
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625 SDSPLSTENFTASG 638
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Matches 7; Conservative
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Best Local Similarity 58.3
Matches 7; Conservative
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                                                                                                             1 RNDSPIQTDQYT 12
                                                                                                                                                                                        41 REDPPVKTTQYT 52
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Best Local Similarity
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gene G protein - phage alpha-3
CiSpecies: phage alpha-3
CiSpecies: phage alpha-3
CiDate: 10-Mar-1994 #sequence revision 10-Mar-1994 #text_change 09-Jul-2004
CiAccession: 822331; C04253, R04253
R; Kodaira, K.I.; Nakano, K.; Okada, S.; Taketo, A.
Biochim. Biophya. Acta 1130, 277-288, 1992
A;Title: Nucleotide sequence of the genome of the bacteriophage alpha3: interrelationshi
A;Reference number: S22324; MUID:92223109; PMID:1532908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Cross-references: UNIPROT:P31281; UNIPARC:UPI0000113352; EMBL:X60322; NID:g14775; PIDN R;Sims, J.; Capon, D.; Dressler, D. N. Biol. Chem. 254, 12615-12628, 1979
A,Fitle: dnaG (primase)-dependent origins of DNA replication. Nucleotide sequences of th A,Reference number: A92247; MUID:80049950; PMID:387790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 165-187 <SIM>
A;Cross-references: UNIPARC:UP1000000389; GB:J02444; GB:M10725; NID:g166103; PIDN:AAA32
C;Comment: This protein is one of the structural components of the bacteriophage capsid.
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R;Ouetier, F.; Rieger, M.; Gabel, C.; Mueller-Auer, S.; Schaefer, M.; Zipp, M.; Salanoub Submitted to the Protein Sequence Database, May 1999
A;Reference number: Z16409
A;Accession: T08408
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Msesidues: 1-294 <QUE>
A;Residues: 1-294 <QUE>
A;Cross-references: UNIRROT: Q9SVL2; UNIPARC: UPI00000A322F; EMBL: AL049862; GSPDB:GN00061;
A;Experimental source: cultivar Columbia; BAC clone F18B3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transcription factor homolog F18B3.150 - Arabidopsis thaliana C,Species: Arabidopsis thaliana (mouse-ear cress) C,Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change
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                    Score 39; DB 2
Pred. No. 19;
6; Mismatches
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Pred. No. 33;
2; Mismatches
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                          40.0%; Score 39;
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ilarity 75.0%;
Conservative
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8 KHDTAIQTSRFSVTG 22
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Best Local Similarity 40.v.
6; Conservative
                                                                                Conservative
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Query Match
Best Local Similarity
6, Conserve
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Best Local Similarity
6; Conserve
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A; Residues: 1-187 < KOD>
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A;Introns: 172/3
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                                                                                                                                                                                                                                                                      A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Rossiues: 1-725,'L' <MI2>
A;Cross-references: UNIPARC:UPI0000062253; EMBL:X63105; NID:g37257; PIDN:CAA44819.1; PIL
R;King, H.W.S.; Tempost, P.R.; Merrifield, K.R.; Rance, A.J.
A;Ring, H.W.S.; Tempost activate met and raf.
A;Title: Tpr.homologues activate met and raf.
A;Reference number: S00928; MUID:88262257; PMID:3387099
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Cispecies: phage phi-K
Cispecies: phage phi-K
Cipate: 15-Aug-1996 #sequence_revision 15-Oct-1996 #text_change 09-Jul-2004
CiAccession: JC4806; B04253; A04253
R;Kodaira, K.; Oki, M.; Kakikawa, M.; Kimoto, H.; Taketo, A.
J. Biochem. 119; 1062-1069; 1996
A;Title: The virion proteins encoded by bacteriophage phi-K and its host-range mutant ph
A;Reference number: JC4804; MUID:96424987; PMID:8827438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-31, R', 33-142 <KIN>
A; Cross-references: UNIPARC:UPI000016B112; EMBL:Y00672; NID:g37255; PIDN:CAA68681.1; PIE
R; Greco, A.
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                    A; Residues: 1-2094 - MITS
A; Cross-references: UNIPROT:Q15624; UNIPROT:Q9UE33; UNIPARC:UPI000017CBF3; EMBL:X66397;
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
R; Mitchell, P.J.; Cooper, C.S.
A; Mitchell, P.J.; Cooper, C.S.
A; Title: Nucleotide sequence analysis of human tpr cDNA clones.
A; Reference number: $23740; MUID:92195670; PMID:1549355
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X;Residues: 165-187 <SIM>
A;Cross-references: UNIPARC:UPI00009COFB
C;Comment: This protein is one of the structural components of the bacteriophage capsid.
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A;Cross-references: UNIPROT:Q38042; UNIPARC:UPI0000138658; EMBL:X60323; NID:g1478118; R;Sims, J; Capon, D.; Dressler, D.
J. Biol. Chem. 254, 12615-12628
A;Title: dnaG (primase)-dependent origins of DNA replication. Nucleotide sequences of A;Reference number: A92247; MUID:80049950; PMID:387790
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Pred. No. 2e+02;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library, December 1995
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A;Status: translated from GB/EMBL/DDBJ
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A; Introns: 177/3
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A; Residues: 144-228 <GRE>
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JC4806
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Length 294;

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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: F80804
R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sprin Nature 402, 769-777, 1999
                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT: Q9M0T2; UNIPARC: UPI000009E989; GB:NC_001268; NID: 97267490; P
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NyAlternate names: RNA nucleotidyltransferase (RNA-directed); RNA replicase
NyOcontains: RNA-directed RNA polymerase (EC 2.7.7.48)

C;Species: canine distemper virus
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: 445389

R;Sidhu, M.S.; Menonna, J.P.; Cook, S.D.; Dowling, P.C.; Udem, S.A.
Virology 193, 50-65, 1993
A;Title: Canine distemper virus L gene: sequence and comparison with related viruses.
A;Reference number: A45389; MUID:93174968; PMID:8438885
A;Accession: A45389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-940 cANT>
A;Residues: 1-940 cANT>
A;Cross-references: UNIPROT:081471; UNIPARC:UPI00009DA3B; EMBL:AF076275; NID:g3293582;
A;Experimental source: cultivar Columbia
                                                                                                                                                         A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana. A;Reference number: A85001; MUID:20083488; PMID:10617198
A;Accession: F85084
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 09-Jul-2004
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athila-like protein [imported] - Arabidopsis thaliana
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1; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          submitted to the EMBL Data Library, August 1998 A; Description: The sequence of A. thaliana TISF16. A; Reference number: Z14443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ore 39; DB;
ed. No. 71;
Mismatches
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Pred. No.
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Best Local Similarity
8; Conserve
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Best Local Similarity
The B; Conserve
                                                                                                                                                                                                                                                                   A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-587 <STO>
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R; Antoniou, B.; Le,
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                                                                                                                                                                                                                                                                                                                                                                                             C;Genetics:
A;Gene: AT4g08490
A;Map position: 4
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Hemagglutinin precursor - influenza A virus

hemagglutinin precursor - influenza A virus

N;Contains: hemagglutinin HA1; hemagglutinin HA2

C;Species: influenza A virus

C;Date: 31-Mar-1993 #sequence revision 31-Mar-1993 #text_change 16-Jun-2000

C;Accession: B39987; A04067; F33157

R;Nobusawa, B:; Aoyama, T:; Kato, H:; Suzuki, Y.; Tateno, Y.; Nakajima, K.

N;Inclocy 182, 475-485, 1991

A;Title: Comparison of complete amino acid sequences and receptor-binding properties amc

A;Reference number: A39987; MUID:91220697; PMID:2024485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: genomic RNA
A; Residues: 1-38, Tu', 40-51, G', 53-101 <AIR>
A; Residues: 1-38, Tu', 40-51, G', 53-101 <AIR>
A; Cross-references: UNIPARC: UPIO000170F31, GB:J02104; NID:g324135; PIDN:AAA43180.1; PID:
A; Experimental source: strain A/duck/Alberta/60/76 [H12]
A; Note: the signal sequence and the amino end of the HA1 chain comprise residues 1-17 and GGenetics:
A; Map position: segment 4
C; Superfamily: influenza virus hemagglutinin, homortimer; transmembrane protein
C; Superfamily: influenza virus hemagglutinin, homortimer; transmembrane protein
F; 18-342/Product: hemagglutinin HA1 #status predicted <HA1>
F; 18-342-544/Product: hemagglutinin HA2 #status predicted <HA2>
F; 343-554/Product: hemagglutinin HA2 #status predicted <HA2>
F; 353-551/Domain: transmembrane #status predicted <HA2>
F; 353-551/Domain: transmembrane #status predicted <HA2>
F; 37, 28, 140, 151, 152, 222, 302, 309, 496, 523/Binding site: carbohydrate (Asn) (covalent) #sta
                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:Q40827; UNIPARC:UPI00000A1FF5; EMBL:U48831; NID:g1431871; PI
C;Superfamily: DNA-binding protein WRKY1
C;Keywords: DNA binding
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Proc. Natl. Acad. Sci. U.S.A. 78, 7639-7643, 1981
A;Itle: Sequence relationships among the hemagglutinin genes of 12 subtypes of influenz A;Reference number: A93902; MUID:82150925; PMID:6174976
A;Accession: A04057
                                                                                       C;Species: Petroselinum crispum (parsley)
C;Date: 12-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 31-Dec-2004
C;Accession: 872443
R;Rushton, P.J; Tovar Torres, J.; Parniske, M.; Wernert, P.; Hahlbrock, K.; Somssich, I R;Rushton, P.J; 5690-5700, 1996
A;Title: Interaction of elacitor-induced DNN-binding proteins with elicitor response eleantemence number: 872443; MUID:97051827; PMID:8896462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPARC:UPI000012C4D8; GB:D90307; NID:g221309; PIDN:BAA14337.1; PID:
A;Experimental source: strain A/duck/Alberta/60/76 [H12N5]
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Pred. No. 68;
2; Mismatches
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DNA-binding protein WRKY1 - parsley
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A; Residues: 1-514 <RUS>
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RESULT 13

C;Genetics: A;Gene: L C;Superfamily: parainfluenza virus RNA-directed RNA polymerase C;Keywords: ATP; nucleotidyltransferase; RNA biosynthesis; RNA replication Query Match
48.1%; Score 39; DB 1; Length 2161;
Best Local Similarity 63.6%; Pred. No. 3.1e+02;
Matches 7; Conservative 1; Mismatches 3; Indels

2 NDSPIQTDQYT 12 || || || || || 1 1656 NDKPILIDQYS 1666

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Search completed: August 30, 2006, 04:30:58 Job time: 9.93939 secs

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Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- permanent accession numbers. The new UniProt record may not contain the previous temporary accession number numbers from the most recent version of UniProt. These sequences have been assigned new Please note that the curators of the UniProt database have purged some temporary accession
- accession number can be found by searching the old accession number in the UniProt Protein extension .rup) that can no longer be found in the database, the permanent record with the new If you encounter an accession number from an older search run against UniProt (results file Archive database (UniPARC) at:

http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher

numbers. members of the public who may encounter UniProt temporary accession include a copy of this attachment to assist any future Examiners or When submitting sequence search results for scanning into IFW, please This Page Blank (uspto)

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Bacteria; Proteobacteria; Gammaproteobacteria; Oceanospirillales;
Hahellaceae; Hahella.
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nes 8; Conserv
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GenCore version 5.1.9 (c) 1993 - 2006 Biocceleration Ltd.
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Q2VBU8_9BACT
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Q2SB97_9GAMM
Q47PF1_THEFY
Q6FJW7_CANGA
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Q4N289 THEPA
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Maximum Match 100%
Listing first 45 summaries
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                                                            protein search, using sw model
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Q8W105_A
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Q8TM75_1
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Q3PUR9
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                                                                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
                                                                                                                                                                                       1 RNDSPIQTDQYTTTG 15
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length: 2000000000
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Match Length DB
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Maximum DB
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	10 10 0	Q5qv82 idiomarina Q6jws3 uncultured P53753 saccharomvo		
2 Q8RBP9_THETN 2 Q8A518_BACTN	2 Q5TRD3_ANOGA 2 Q757X1_ASHGO 2 Q6FN92_CANGA	2 Q5QV82_IDILO 2 Q6JWS3_9BACT 1 ENG1 YEAST	2 Q3RSQ2 RALME 2 Q60SS8 CABBR 2 Q5WCK0 BACSK	2 Q7RUA3_NEUCR 2 Q56PA2_9METZ 2 Q54Z36_DICDI
339	414 429 662	713 860 1117	97 99 213	234 236 255
50.6	50.6 50.6 50.6	50.6	4 4 4	4.004 4.004 4.4.4.
41	4 4 4	444	4 4 4	0 4 4 0 4 0 0 0
32	8 8 8 8 8 8	37 38 39	4 4 4 0 H S	4 4 4 6 4 6

ALIGNMENTS

Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License NUCLEOTIDE SEQUENCE.
Liu F., Lu J., Hu W., Wang S.-Y., Cui S.-J., Chi M., Yan Q.,
Kang K.-R., Song H.-D., Xu X.-N., Wang J.-J., Zhang X.-L., Wang Z.-Q.,
Xue C.-L., Brindley P.J., McManus D.P., Yang P.-Y., Feng Z., Chen Z.,
Han Z.-G.; 07-FEB-2006, entry version 3. SJGGG06457 protein (Fragment). Schistosoma japonicum (Blood fluke). Bukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma. Gaps "New Perspectives on Host-parasite Interplay by Comparative Transcriptomic and Proteomic Analyses of the Human Blood Fluke, Schistosoma japonicum."; Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases. ö 59.3%; Score 48; DB 2; Length 196; 57.1%; Pred. No. 5.4; 1.1ve 4; Mismatches 2; Indels 196 AA; 21675 MW; CO4EF1B36AFFAA87 CRC64; 08-NOV-2005, integrated into UniProtKB/TrEMBL 08-NOV-2005, sequence version 1. 196 AA. ЕМВL; AY809222; ABA40295.1; -; mRNA. NON_TER 196 196 PRT; PRELIMINARY; 2 NDSPIQIDOYTTIG 15 Conservative

SNSPVKTKQYETTG 144

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24-JAN-2006, integrated into UniProtKB/TrEMBL. 24-JAN-2006, sequence version 1. 07-FEB-2006, entry version 2. ORFNames-HCH_05408; 363 AA PRT; QZSB97_9GAMM PRELIMINARY; Q2SB97;

Lyase

SWARACCCCRTTABARKS

Matches

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Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla B.,
Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
Boisrame A., Robre E., Fairhead C., Ferry Jonazet H., Groppi A.,
Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
M. Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
Nicaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
A Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,
Zeniou-Meyer M., Zivanovic Y., Bolotin-Pukuhara M., Thierry A.,
A Bouchler C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
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Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein (By
                                                                                                                             Candida glabrata (Yeast) (Torulopsis glabrata).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
MCBI_TaxID=5478;
                                     19-UUL-2004, sequence version 1.
21-FEB-2006, entry version 18.
Candida glabrata strain CBS138 chromosome M complete sequence.
OrderedLocusNames=CAGLOM3003g;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-0CT-2005, integrated into UniProtKB/TrEMBL.
11-0CT-2006, sequence version 1.
11-0CT-2006, entry version 4.
Hypothetical protein.
OrderedLocusNames=Nwi 3082; ORFNames=Nwi 3082;
Butrobacter winogradskyi (strain Nb-255 \( 7\) ATCC 25391).
Bracteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Bradyrhizobiaceae; Nitrobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complete proteome; Membrane; Transmembrane; Transport. SEQUENCE 558 AA; 61177 MW; 05760736C33F432D CRC64;
                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
STRAIN=ATCC 2001 / CBS 138;
PubMed=15229592; DOI=10.1038/nature02579;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
                  19-JUL-2004, integrated into UniProtKB/TrEMBL
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GO, GO:0016021; C:integral to membrane; IEA.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0005215; F:transporter activity; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IPR007114; MFS.
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1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54.3%; Score 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Genome evolution in yeasts.";
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Q3SN12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VS DOB Joint Genome Institute;
Copeland A., Lucas S., bapidus A., Barry K., Detter J.C., Glavina T.,
Hammon N., Israni S., Pitluck S., Di Bartolo G., Chain P., Schmutz J.,
Larimer F., Land M., Lykida A., Richardson P.;
"Complete sequence of Thermobifida fusca YX.";
Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
STRAIN=KCTC 2396;
PubMed=16552867; DOI=10.1093/nar/gki1016;
Jeong H., Yim J.H., Lee C., Choi S.-H., Park Y.K., Yoon S.H.,
Hur C.-G., Kang H.-Y., Kim D., Lee H.H., Park K.H., Park S.-H.,
Park H.-S., Lee H.K., Off T.K., Kim J.F.;
"Genomic blueprint of Hahella chejuensis, a marine microbe producing
                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-SEP-2005, sequence version.
13-SEP-2006, entry version 4.

O7-FEB-2006, entry version 4.

Putative solute-binding dependent transport lipoprotein precursor.
OrderedLocusNames=Tfu 1633;
Thermobifida fusca (strain YX).
Streptosporangineae; Actinobacteriae, Actinomycetales;
Streptosporangineae; Nocardiopsaceae; Thermobifida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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                                                                                                                                                                                                                                                                                                                                                                                 56.8%; Score 46; DB 2; Length 363; 53.3%; Pred. No. 25; 13%; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                       363 AA; 41267 MW; 8A2619C94CC8D185 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
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64.3%; Pred. No. o.,
0, Mismatches
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GO; GO:0005215; F:transporter activity; IEA
GO; GO:0006810; P:transport; IEA.
                                                                                                                                                                                                                                                 EMBL; CP000155; ABC32077.1; -; Genomic_DNA.
GO; GO:0016829; F:lyase activity; IEA.
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                                                                                                                                                           Nucleic Acids Res. 33:7066-7073 (2005)
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Pfam; PF00496; SBP bac 5; 1.
PRINTS; PR01415; ANKYRIN.
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                                                                                                                                    an algicidal agent."
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RESULT 3

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Gaps

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Matches

RESULT 4 Q6FJW7 CA ID Q6FJ

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Length 558; 5; Indels

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Query Match
Best Local S
Matches 8
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Distributed under the Creative Commons Attribution-NoDerivs License
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ORFManes-CaurDRAFT 1873;
Chloroflexus aurantiacus J-10-fl.
Bacteria, Chloroflexi, Chloroflexases, Chloroflexus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US DOE Joint Genome Institute (JGI-PGF);
Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T.,
Hammon N., Israni S., Pitluck S., Richardson P.;
Submitted (SEP-2005) to the EMBL/GenBank/DDBJ databases.
Hammon N., Israni S., Pitluck S., Chain P., Malfatti S., Shin M., Vergez L., Schmutz J., Larimer F., Land M., Hauser L., Kyripides N., Lykidis A., Richardson P.; "Complete sequence of Nitrobacter winogradskyi Nb-255."; Submitted (SEP-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    53.7%; Score 43.5; DB 2; Length 515; 60.0%; Pred. No. 1e+02; 1ive 2; Mismatches 3; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to the EMBL/GenBank/DDBJ databases
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Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                  PRINTS; PRO0507; NIZNGWTERASE.
PROSITE; PS00092; NG MTASE; UNKNOWN 1.
Complete proteome; Hypothetical protein.
SRQUENCE 515 AA; 54223 MW; 4F973B39D823E669 CRC64;
                                                                                                                                                                                                EMBL; CP000115; ABA06329.1; -; Genomic_DNA.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0008170; F:N-methyltransferase activity; IEA.
GO; GO:000306; P:DNA methylation; IEA.
InterPro; IPR002296; N12NE mtfrase.
InterPro; IPR002052; N6_Mtase.
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US DOB Joint Genome Institute (JGI-PGF);
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QJDWSS;
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SUBJECT 6

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The Pubmed-15466914; DOI-10.1038/nature03025;

A Jaillon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,

Andredi E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,

Anicaud S., Jaffe D., Fischer S., Lutfalla G., Dossat C., Segurens B.,

Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,

Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,

Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,

Anthouard V., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J.,

Rellis M., Volff J.-N., Gilgo R., Zody M.C., Mesirov J.,

An Lindblad-Toh K., Birren B., Nubsum C., Kahn D., Robinson-Rechavi M.,

Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,

Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.,

"Genome duplication in the teleost fish Tetraodon nigroviridis reveals

"" Nature 431:946-957(2004).
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Distributed under the Creative Commons Attribution-NoDerivs License
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Actinopterygii, Neopterygii, Teleostei, Buteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes;
Tetradontoidea, Tetraodontidae, Tetraodon.
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-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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0
                                                                                                                                                                                                                                                    53.1%; Score 43; DB 2; Length 310; 53.3%; Pred. No. 70;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chromosome 13 SCAF14566, whole genome shotgun sequence. ORFNames=GSTENG00016807001;
                                                                                                                                                                                        EDB84C3A58A4E6B7 CRC64;
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SEQUENCE 340 AA; 36745 MW; 1E282568C07674E5 CRC64;
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                                                                                      EMBL; AAAH02000045; EAOS7904.1; -; Genomic DNA.
GO; GO:0016740; F:transferase activity; IEĀ.
GO; GO:0009058; P:biosynthesis; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-JUL-2005, integrated into UniProtKB/TrEMBL
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Pred. No. 78;
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                                                                                                                                                                                        310 AA; 33946 MW;
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53.3%;
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nes 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=2225576; PubMed=12368865; DOI=10.1038/nature01099; Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M., Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L., Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L., Shallom S.J., van Aken S.E., Riedmuller S.B., Feldbiyum T.V., Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M., Florens L., Yaces J.R. III, Rahim J.D., Sinden R.E., Harris M.A., van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R., Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
Zhang Y.-Q., Ren S.-X., Li H.-L., Wang Y.-X., Fu G., Yang J., Qin Z.-Q., Miao Y.-G., Wang W.-Y., Chen R.-S., Shen Y., Chen Z., Yuan Z.-H., Zhao G.-P., Qu D., Danchin A., Wen Y.-M.; Glaconea-based analysis of virulence genes in a non-biofilm-forming Staphylococcus epidermidis strain (ATCC 12228)."; Mol. Microbiol. 49:1577-1593(2003).
                                                                                                                                                                                                                                                                                                                                      EMBL, AE015929; AAO05900.1; -; Genomic_DNA.
BioCyc; SEP1176280:SE2258-MONOMER; -.
GO; GO:0016788; F:hydrolase activity, acting on ester bonds; IEA.
GO; GO:0046972; F:metal ion binding; IEA.
GO; GO:000166; F:mucleotide binding; IEA.
GO; GO:000166; P:nucleotide catabolism; IEA.
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 43; DB 2; Length 511
Pred. No. 1.2e+02;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PROIGO7; APYRASEFAMLY.
PROSTITE; PSO0786; 5 NUCLEOTIDASE 2; 1.
COMPLETE protecome; Metal-binding; Nuclectide-binding.
SEQUENCE 511 AA; 57798 MW; 47487BE2096ADEC6 CRC64;
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15-DEC-2003, sequence version 1.
21-FEB-2006, entry version 15.
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Interpro; IPR006146; 5'-Nucleotdase_N.
Interpro; IPR006149; 5 'Nucleotidase.
Interpro; IPR004843; M-pesterase.
PANTHER; PTHR11575; 5 nucleotidase; 1.
Pfam; PP02872; 5 nucleotidase; 1.
Pfam; PP0249; Metallophos; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   parasite Plasmodium yoelii yoelii.";
Nature 419:512-519(2002).
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66.7%;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLECTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

Pubmed=15774886; DOI=10.1128/JB.187.7.2426-2438.2005;

Adil S.R., Foults D.E., Archer G.L., Mongodin E.F., DeBoy R.T.,

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Dodson R.J., Daugherty S.C., Madupu R., Angluoli S.V., Durkin A.S.,

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Hance I.R., Nelson K.E., Fraser C.M.;

"Insights on evolution of virulence and resistance from the complete
genome analysis of an early methicillin-resistant Staphylococcus
granten sarain and a biofilm-producing methicillin-resistant
Staphylococcus epidermidis strain..;

J. Bacteriol. 187:2426-2438(2005).
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                                                                                                                                                                                                                                                                                                                                                        Staphylococcus epidermidis (strain ATCC 35984 / RP62A).
Bacteria, Firmicutes, Bacillales, Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00786; 5 NUCLECTIDASE 2; 1.
Complete protecome; Metal-binding; Nucleotide-binding.
SEQUENCE 511 AA; 57848 MW; F160793204D4149C CRC64;
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PubMed=12950922; DOI=10.1046/j.1365-2958.2003.03671.x;
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07-FEB-2006, entry version 20.
Lactococcal phosphatase-like protein.
OrderedLocusNames=SE258, ORFNames=SE 2258;
Staphylococcus epidermidis (strain ATC 12228).
Bacteria; Firmiqutes; Bacillales; Staphylococcus.
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                                                                                                                    511 AA.
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                                                                                                                    PRT;
                                                                                                         Q5HKQS_STAEQ PRELIMINARY; PRY
Q5HKQ5;
15-PEB-2005, integrated into Unit
15-PEB-2005, sequence version 1.
                                                                                                                                                                                                                                                      07-FEB-2006, entry version 11.
5'-nucleotidase family protein.
OrderedLocusNames=SERP2288;
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Rhabditidae; Peloderinae; Caenorhabditis.
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MEDLINE=99069613; PubMed=9851916; DOI=10.1126/science.282.5396.2012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cottrell M.T., Yu L., Kirchman D.L., Sakoquence and Expression Analyses of Cytophaga-Like Hydrolases in Western Arctic Metagenomic Library and the Sargasso Sea."; Appl. Environ. Microbiol. 71:8506-8513 (2006).
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                                                                                                                                                                                    53.1%; Score 43; DB 2; Length 516; 54.5%; Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 43; DB 2; Length 634
Pred. No. 1.6e+02;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                     2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-JAN-2006, integrated into UniProtKB/TrEMBL.
10-JAN-2006, sequence version 1.
07-FEB-2006, entry version 3.
FTX toxins and related Ca2+-binding protein (Fragment).
uncultured Bacteroidetes bacterium 'SB12-18 P41A3'.
Bacteria; Bacteroidetes; environmental samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tavernarakis N., Shreffler W., Wang S.L., Driscoll M.; Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                          62120 MW; 8CBA858FA3C373FC CRC64;
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                       EMBL, AABL01001174; EAA15729.1; -; Genomic_DNA
GO; GO:0016829; F:lyase activity; IEA.
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NON TER 634 634
                                                                                                                                                                                                                                                            3; Mismatches
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Caenorhabditis elegans.
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61.5%;
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les 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Da Lage J.-L., Van Wormhoudt A., Cariou M.-L.;
"Diversity and evolution of the alpha-amylase genes in Animals.";
Biologia 57:181-189(2002).
Potential.
Cytoplasmic (Potential).
N-linked (GlcNAc. .) (Potential).
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Bukaryota, Metazoa, Mollusca, Bivalvia, Heteroconchia, Veneroida,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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Da Lage J.L., Feller G., Janecek S.;
"Horizontal gene transfer from Eukarya to bacteria and domain shuffling: the alpha-amylase model.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 43; DB 1; Length 664;
Pred. No. 1.7e+02;
0; Mismatches 2; Indels
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/FTId=PRO 0000181285.
Cytoplasmic (Potential).
Potential.
Extracellular (Potential).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2003, integrated into UniProtKB/TrEMBL. 05-JUL-2004, sequence version 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       699 AA.
                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U76403; AAB39735.1; -; mRNA.
EMBL; Z68003; CAA91975.1; -; Genomic_DNA.
PIR; T20420; T20420.
Ensembl; E02H4.1; Caenorhabditis elegans.
WormBase; WBGene00000952; del-1.
WormPep; E02H4.1; CE05547.
InterPro; IPR004126; Deg-1.
InterPro; IPR004126; Deg-1.
PANTHER; PTHR11690; Na+channel_ASC.
PANTHER; PTHR11690; Na+channel_ASC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Corbiculoidea; Corbiculidae; Corbicula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR01078; AMINACHANNEL.
TIGRFAMB; TIGR00867; deg-1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75474 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53.1%;
80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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88
607
607
628
664
241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=45949;
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ORIPPE SBLVA

DT 01-MAR-2003, in

DT 07-FEB-2006, en

DE Alpha-amylase.

GN Name-Amy;

CC Corbicula flumi

CC Carbicula flumi

RN (2)

RN (4)

RN (5)

RN (6)

RN (7)

RN (7)

RN (1)

RN (1
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completed: August 30, 2006, 04:29:24
ne : 61.4848 secs
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Job time :
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100000000888
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                                                                                                                                                                    Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-Muguga;
PubMed=15994558; DOI=10.1126/science.1110439;
Budmed=15994558; DOI=10.1126/science.1110439;
Gardner M.J., Bishop R., Shah T., de Villiers E.P., Carlton J.M.,
Hall N., Ren Q., Pauleen I.T., Pain A., Berriman M., Wilson R.J.,
Sato S., Ralph S.A., Mann D.J., Xiong Z., Shallom S.J., Weidman J.,
Jiang L., Lynn J., Weaver B., Shoabib A., Domingo A.R., Wassawo D.,
Crabtree J., Wordman J.R., Fasabib A., Domingo A.R., Pertea M.,
Suh B., Silva J.C., Utterback T.R., Feldblyum T.V., Pertea M.,
Allen J., Nierman W.C., Taracha B.L., Salzberg S.L., White O.R.,
Fitzhugh H.A., Morzaria S., Venter J.C., Fraser C.M., Nene V.;
"Genome Sequence of Theileria parva, a Bovine Pathogen That Transforms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=Muguga;
Gardner M., Bishop R., Shah T., de Villiers E., Carlton J.M., Hall N.,
Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.M., Sato S.,
Ralph S.A., Mann D.J., Xiong Z., Shallom S.J., Weidman J., Jiang L.,
Lynn J., Weaver B., Shoaibi A., Wasawo D., Crabtree J., Wortman J.R.,
Haas B., Angiuoli S., Creasy T.H., Lu C., Suh B., Silva J.C.,
Salzberg S.L., White O., Fitzhugh H.A., Morzaria S., Venter J.C.,
Fraser C.M., Nene V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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0
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                                                                                                                     - - SIMILARITY: Belongs, to the glycosyl hydrolase 13 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53.1%; Score 43; DB 2; Length 699; 46.7%; Pred. No. 1.8e+02; ive 5; Mismatches 3; Indels
                                                                          Da Lage J.-L.;
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00642; Aamy; 1.
SMART; SM00632; Aamy C; 1.
ernirence 699 AA; 76544 MW; 25D57008165B04CB CRC64;
                                                                                                                                                                                                                                                                     HSSP; P04745; ISMD.

GO; GO: 0004556; P: Alpha-amylase activity; IEA.

GO; GO: 0005597; P: Carbohydrate metabolism; IEA.

InterPro; IPR006589; Alp_amyl_cat_sub.

InterPro; IPR006048; Alpha_amyl_c.

InterPro; IPR006048; Alpha_amyl_cat.

InterPro; IPR006047; Alpha_amyl_cat.

Pfam; PF000128; Alpha-amylase; 1.

Pfam; PF000128; Alpha-amylase; 2.

PRINTS; PR00110; ALPHAAMYLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-AUG-2005, integrated into UniProtKB/TrEMBL. 02-AUG-2005, sequence version 1. 07-FBE-2006, entry version 3. 07-FBE-2006, entry version 3. 08-FNames=TP04_0468;
                                                                                                                                                                                                                                                 EMBL; AF468016; AAO17927.2; -; Genomic_DNA.
Cell. Mol. Life Sci. 61:97-109(2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 QSNEPIKTSÖYTSLG 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 RNDSPIQTDQYTTTG 15
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                                                   NUCLEOTIDE SEQUENCE
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hes 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Theileria parva
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Q4N289;
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                                                                                                                                    Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMede15994597, DOI=10.1258/jrsm.98.7.320;
Pain A., Renauld H., Berriman M., Murphy L., Yeats C.A., Weir W., Kernornou A., Aslett M., Eishop R., Bouchier C., Cochet M., Coulson R.M.R., Cronin A., de Villiers B.P., Fraser A., Fosker N., Gardner M., Goble A., Griffiths-Jones S., Harris D.E., Katzer F., Larke N., Lord A., Maser P., McKellar S., Mooney P., Morron F., Nene V., O'Neil S., Pric C., Quail M.A., Rabbinowitsch E., Rawlings N.D., Rutter S., Saunders D., Seeger K., Shah T., Squares S., Tivey A., Walker A.R., Woodward J., Dobbelaere D.A.E., Langsley G., Rajandream M.A., McKeever D., Shiels B., Tait A., "Genome of the host-cell transforming parasite Theileria annulata
                          -!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileriidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 5261;
                                                                                                                                                                                                 EMBL; AAGKO10000004; EAN31820.1; -; Genomic_DNA.
Hypothetical protein.
SEQUENCE 809 AA; 92620 MW; S8FA8368C3613471 CRC64;
                                                                                                                                                                                                                                                                                                                                     Length 809;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53.1%; Score 43; DB 2; Length 520.
63.8%; Pred. No. 1.7e+03;
63.8%; Pred. No. 1.7e+03; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SfiI-subtelomeric related protein family member, putative
                                                                                                                                                                                                                                                                                                                                                                                             4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          603934 MW; 79941BB66659B78E CRC64;
Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                  53.1%; Score 43; DB 2; I
50.0%; Pred. No. 2.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-UUL-2005, integrated into UniProtKB/TrEMBL. 05-JUL-2005, sequence version 1. 07-FEB-2006, entry version 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; CR940348; CA174027.1; -; Genomic_DNA.
InterPro; IPR013320; Cona_like_subgrp.
Pfam; PF04385; FAINT; 54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 5261 AA.
                                                                                                                                                                                                                                                                                                                                                                                          3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=Ankara isolate clone C9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kinase, Repeat, Transferase
SEQUENCE 5261 AA; 603934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4887 NDNPLTKNDYTTT 4899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         526 NNSPISNSEFITIG 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 NDSPIQTDQYTTTG 15
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Best Local Similarity 53.c.
7; Conservative
                                                                                                                                                                                                                                                                                                        Ouery Match
Best Local Similarity 50.v.
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         compared with T. parva.";
Science 309:131-133(2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 NDSPIQTDQYTTT 14
                                                                                  preliminary data.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORFNames=TA16050;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=5874;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q4UFT9_THEAN
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Sequence:

6

Run

Searched:

Database

Result

48.9

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Sequence 5, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 38395, A
Sequence 38195, A
Sequence 19132, A
Sequence 19132, A
Sequence 1579, Ap
Sequence 1780, Ap
Sequence 1780, Ap
Sequence 1780, Ap
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3702-37.
Sequence 3734287
Facet No. 6734287
GENERAL INPORMATION:
APPLICANT: Lawton, Robert
APPLICANT: Lawton, Robert
APPLICANT: Prancoeur, Greg
TITLE OF INVENTION: Specific Binding Protein for Treating;
FILE REFERENCE: 01-125A
CURRENT APPLICATION NUMBER: US/09/281,760E
CURRENT APPLICATION NUMBER: 09/058,331
PRIOR APPLICATION NUMBER: 09/058,331
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 39
NUMBER OF SEQ ID NOS: 39
                                            US-08-455-838-5

US-09-019-809-5

US-09-220-806-5

US-09-270-767-38395

US-09-270-767-38395

US-09-270-767-53612

US-09-248-796A-19132

US-09-248-796A-19132

US-09-248-796A-15409

US-09-248-796A-15409

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US-09-248-796A-15409

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US-09-2710-279-17700
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LOCATION: (136)..(136)
OTHER INFORMATION: "n" stands for any nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
MAME/KEY: misc feature
LOCATION: (451)..(451)
OTHER INFORMATION: "n" stands for any nucleic acid
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LOCATION: (568)..(568)
OTHER INFORMATION: "n" stands for any nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (530)..(530)
OTHER INFORMATION: "n" stands for any nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for any nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                   US-09-634-238-335
US-09-248-796A-21802
US-09-844-006A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALIGNMENTS
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NAME/KEY: misc_feature
LOCATION: (413)..(414)
OTHER INFORMATION: "n" stands for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEX: misc feature
LOCATION: (500). (500)
OTHER INFORMATION: "n" stands
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            stands
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 37
LENGTH: 108
TYPE: PRT
ORGANISM: Canis familiaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: misc feature
LOCATION: (460)..(462)
OTHER INFORMATION: "n"
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NAME/KEY: misc feature
US-09-281-760E-37
\begin{array}{c} \mathbf{n} \\ \mathbf{
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61, Appl
63, Appl
59, Appl
10828, A
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14, Appli
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4053, Appl
43446, Ap
4294, Ap
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Sequence 2, Appli
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                                                                                                                                                                      August 30, 2006, 04:31:13 ; Search time 14.8485 Seconds (without alignments) 88.424 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /BMC_Celerra_SIDS3/ptodata/2/jaa/5_COMB.pep:*
/BMC_Celerra_SIDS3/ptodata/2/jaa/6_COMB.pep:*
/BMC_Celerra_SIDS3/ptodata/2/jaa/7_COMB.pep:*
/BMC_Celerra_SIDS3/ptodata/2/jaa/H_COMB.pep:*
/BMC_Celerra_SIDS3/ptodata/2/jaa/PCTUS_COMB.pep:*
/BMC_Celerra_SIDS3/ptodata/2/jaa/RC_COMB.pep:*
/BMC_Celerra_SIDS3/ptodata/2/jaa/RC_COMB.pep:*
/BMC_Celerra_SIDS3/ptodata/2/jaa/RC_COMB.pep:*
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                     GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-09-479-614-14
US-09-479-614-2
US-09-479-614-29
US-09-134-001C-4053
US-09-134-001C-4053
US-09-206-942-65
US-09-206-942-65
US-09-206-942-63
US-09-206-942-63
US-09-206-942-63
US-09-206-942-63
US-09-238-016-10828
US-09-238-016-10828
US-09-238-016-10828
US-09-6108-809-7
US-08-532-547-9
US-09-019-809-9
US-09-019-809-9
US-09-471-177-9
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US-10-099-285A-72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     650591 segs,* 87530628 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                           OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                           BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                       1 RNDSPIQTDQYTTTG 15
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Maximum DB seq length: 2000000000
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Match Length DB
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667-
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RESULT 4
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Sequence 2, Application US/09701623C

Sequence 2, Application US/09701623C

GENERAL NO. 681170S:

TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF

TITLE OF INVENTION: ALLERGY

FILE REFERENCE: 11514153US1

CURRENT FAPLICATION NUMBER: US/09/701,623C

CURRENT FILING DATE: 2000-12-01

PRIOR APPLICATION NUMBER: PCT/US99/13959

PRIOR PILING DATE: 1999-06-20

PRIOR FILING DATE: 1998-06-20

PRIOR FILING DATE: 1998-06-20

NUMBER OF SEQ ID NOS: 91

SEQ ID NO 2

LENGTH: 312

TABLE OF THE TREATMENT OF THE TREA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
NAME/KEY: misc feature
LOCATION: (847)..(849)
OTHER INFORMATION: "n" stands for any nucleic acid
                                                                                                                        FRATURE:
MAMB/KRY: misc feature
LOCATION: (853)
OTHER INFORMATION: "n" stands for any nucleic acid
                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc feature
LOCATION: (1382)...(1382)
OTHER INFORMATION: "n" stands for any nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature

// LOCATION: (1832)

// COTHER INFORMATION: "n" stands for any nucleic acid

US-09-281-760B-37
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AUTHORS: Patel,
JOURNAL: Immunogenetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08336583; Patent No. 5629415; GENERAL INFORMATION: APPLICANT: HOLLIS, GREGORY F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 RNDSPIOTDOYTTTG 15
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Matches 15; Conservative
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Best Local Similarity
Matches 15; Conserva
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ORGANISM: Dog
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US-09-701-623C-2
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US-08-336-583-2
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Gaps
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APPLICANT: PATEL, MAYUR D.
TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULIN E
NUMBER OF SEQUENCES: 2
NUMBER OF SEQUENCES: 2
ADDRESPONDENCE ADDRESS: 2
ADDRESSEE: ALINCOLN AVENUE
STREET: 126 E. LINCOLN AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: HOLLIS, GREGORY F.
APPLICANT: HOLLIS, GREGORY F.
APPLICANT: APTEL, MAYUR D.
TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULINS;
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHRISTINE B. CARTY
STREET: 126 E. LINCOLM AVENUE; P.O. BOX 2000
                                                                                                                                                                               COUNTRY: USA

ZIP: 0.7065-0900

COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Parentin Release #1.0, Version #1.25
SOFTWARE: Parentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,583
FILING DATE: 09-NOV-1994
CLASSIFICATION: 424
ATTORNEY/ABENT INFORMATION:
NAME: CARTY, CHRISTINE E.
REGISTRATION NUMBER: 36,099
REFERENCE/DOCKET NUMBER: 1921
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-6734
TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: RAHWAY
STATE: NEW JERSEY
COUNTRY: NEW JERSEY
COUNTRY: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13795
FILING DATE:
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ATTORNEY/AGENT INFORMATION:
NAME: CARTY, CHRISTINE B.
REGISTRATION NUMBER: 36,099
REFERRUCE/DOCKET NUMBER: 19211Y
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            357 RNDSPIQTDQYTTTG 371
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Best Local Similarity 100.0
Matches 15; Conservative
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STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                          NEW JERSEY
: USA
                                                                                                                                                 CITY: RAHWAY STATE: NEW JE
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Mismatches
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US-09-270-767-43446
Sequence 43446, Application US/09270767
Parent No. 6703491
GENERAL INFORMATION:
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Best Local Similarity 61.5%;
Matches 8; Conservative
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428 NDSPVRTEQQATT 440
                                                                  428 NDSPVRTEQOATT 440
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Best Local Similarity 58.3°
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8; Conservative
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                                  2 NDSPIQTDQYTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Felis catus US-09-479-614-29
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 Matches
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US-09-479-614-2
; Sequence 2, Application US/09479614
; Sequence 2, Application US/09479614
; Patent No. 6573372
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Exic
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION WUMBER: US/09/479,614
; CURRENT APPLICATION WUMBER: 60/115,033
; EARLIER FULING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
: LENGTH: 496
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Sequence 14, Application US/09479614

Patent No. 6573372

GENERAL INFORMATION:

APPLICANT: WcCall, Catherine

TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
FILER REFERENCE: P-1047

CURRENT APPLICATION NUMBER: US/09/479,614

CURRENT FILING DATE: 2000-01-07

EARLIER APPLICATION NUMBER: 60/115,033

EARLIER FILING DATE: 1999-01-07

NUMBER OF SEQ ID NOS: 34

SOUTWARE: PatentIn Ver. 2.0
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                                                                                                                                                                                       Length 426;
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Pred. No. 3.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 48; DB 2; Length 431;
Pred. No. 3.1;
                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
                                                                                                                                                                                         100.0%; Score 81; DB 5;
100.0%; Pred. No. 5.8e-06;
                                                                                                                                                                                                                            0; Mismatches
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            TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 426 amino acids
TYPE: amino acids
STRANDENNESS: single
(908) 594-6734
                                                                                                                                                                                                                                                                                     357 RNDSPIQTDQYTTTG 371
                                                                                                                                                                                                                                                               1 RNDSPIQTDQYTTTG 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      363 NDSPVRTEQQATT 375
                                                                                                                                                                                     Query Match
Best Local Similarity 100.0
Matches 15, Conservative
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                                                                                                                ; TOPOLOGY: linear;
; MOLECULE TYPE: protein
PCT-US95-13795-2
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ORGANISM: Felis catus
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ORGANISM: Felis catus
US-09-479-614-2
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Best Local Similarity
 TELEPHONE:
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US-09-479-614-14
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Sequence 4012-101.
Sequence 4012-101.
Sequence 4013. Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICAVT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR APPLICATION UNMBER: US 60/055,779
PRIOR APPLICATION STATE 1997-08-14
NUMBER FOR SEQ ID NOS: 5674
SEQ ID NO 4053
LENGTH: 533
                                                                                                                                                    US-09-479-614-29
US-09-479-614-29

Squence 29, Application US/09479614

Patent No. 6573372

GENERAL INFORMATION:

APPLICANT: McCall, Catherine

APPLICANT: Weber, Eric

TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods

FILE REPRENCE: P-1047

CURRENT APPLICATION NUMBER: US/09/479,614

CURRENT FILING DATE: 2000-01-07

NUMBER OF SEQ ID NOS: 34

SOFTWARE: Patentin Ver. 2.0

SQ ID NO 29

LENGTH: 496

TYPE: RRT
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Pred. No. 3.6;
3; Mismatches 2; Indels
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  Indels
  5
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Pred. No. 64;
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Gaps

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RESULT 13
US-09-206-942-63
US-09-206-942-63
Sequence 63, Application US/09206942
Patent No. 6432669
GENERAL INFORMATION:
APPLICANT: LOOSMORE. Sheena M.
APPLICANT: LOOSMORE. Sheena M.
TITLE OF INVENTION: Protective Recombinant Haemophilus Influenzae High
TITLE OF INVENTION: Molecular Weight Proteins
FILE REFERENCE: 1038-861 MIS:jb
CURRENT APPLICATION NUMBER: US/09/206,942
CURRENT APPLICATION NUMBER: 09/167,568
EARLIER PILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 95
SOFTWARE: PatentIN Ver. 2.1
SEQ ID NO 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Loosmore, Sheena M.
APPLICANT: Vang, Yan-Ping
APPLICANT: Yang, Yan-Ping
APPLICANT: Xang, Yan-Ping
APPLICANT: Sang, Yan-Ping
APPLICANT: Klein, Michel H.
TITLE OF INVENTION: PROTECTULAR WEIGHT PROTEINS
TITLE OF INVENTION: MOLECULAR WEIGHT PROTEINS
TITLE OF INVENTION: WOLECULAR WEIGHT PROTEINS
CURRENT APPLICATION WUMBER: US/10/193,764
CURRENT FILING DATE: 2002-07-12
PRIOR PILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 91
SEQ ID NOS: 91
SEQ ID NOS: 10-07
TENTION OF 11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-00-11-0
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Pred. No. 2.4e+02;
6; Mismatches 3; Indels
                       Score 40; DB 2; Length 1180;
Pred. No. 2.4e+02;
6; Mismatches 3; Indels
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40.0%; Pred. No. 2.4e+02;
tive 6; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 61, Application US/10193764
Patent No. 6849447
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Haemophilus influenzae
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                                 49.4%;
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Best Local Similarity 40.0%;
Matches 6; Conservative (
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21 RSDTNLENEEYTGTG 35
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13 RSDTNLENEEYTGTG 27
                                                                                                                                                            1 RNDSPIQTDOYTTIG 15
                                                                                                                                                                                                 13 RSDTNLENEEYTGTG 27
                              Query Match
Best Local Similarity 40.0<sup>3</sup>
Matches 6; Conservative
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Matches 6; Conserv
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Patent No. 6562958

GENERAL INFORMATION:

APPLICANT: GATY L. Breton et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

TITLE OF INVENTION: BAUMANNI FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: BAUMANNI FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT APPLICATION NUMBER: US/09/328,352

SEQ ID NOS: 8252

SEQ ID NO 4294
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APPLICANT: LOCSMOTE, Sheena M.
APPLICANT: LOCSMOTE, Sheena M.
APPLICANT: Ann-Ping
TITLE OF INVENTION: Protective Recombinant Haemophilus Influenzae High
TITLE OF INVENTION: Molecular Weight Proteins
TITLE OF INVENTION: Molecular Weight Proteins
TITLE OF INVENTION: Molecular Weight Proteins
FILE REPERENCE: 1038-861 MIS:ib
CURRENT FILING DATE: 1938-12-08
EARLIER APPLICATION NUMBER: 09/167,568
EARLIER PLING DATE: 1939-10-07
NUMBER OF SEQ ID NOS: 95
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 65
LENGTH: 1180
APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PATENTIN Ver. 2.0
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Pred. No. 1.2e+02;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 40; DB 2; Length 163;
Pred. No. 25;
2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-43446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 65, Application US/09206942
Patent No. 6432669
                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-4294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-09-206-942-65
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Best Local Similarity 50.0%;
Matches 7; Conservative
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Matches 7; Conservative
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LENGTH: 163
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US-09-206-942-65
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US-UN-191-ULO LUBGE APPLICATION US/09949016

PATENT NO. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REPRENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR PLILING DATE: 2000-10-03

PRIOR PLILING DATE: 2000-10-03

PRIOR PLILING DATE: 2000-10-03

PRIOR PLILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

LEMOTH: 2186
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squence 59 Application US/10193764

patent No. 684947

GENERAL INFORMATION:
APPLICANT: Loosmore, Sheena M.
APPLICANT: And, Yan-Ping

APPLICANT: And, Yan-Ping

APPLICANT: Rlein, Michel H.
TITLE OF INVENTION: PROTECTIVE RECOMBINANT HAEMOPHILUS INFLUENZAE HIGH

TITLE OF INVENTION: MOLECTLAR WEIGHT PROTEINS
FILE REFERENCE: 1038-1239MIS

CURRENT APPLICATION NUMBER: US/10/193,764

CURRENT FILING DATE: 1998-10-07

NUMBER OF SEQ ID NOS: 91

SOFTWARE: PATENTIN VOICE: 2.1

SEQ ID NO 59

LENDRY HIBB
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Pred. No. 2.4e+02;
6; Mismatches 3; Indels
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Best Local Similarity 40.0%;
Matches 6; Conservative
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Best Local Similarity 70.0
Matches 7; Conservative
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; ORGANISM: Human
US-09-949-016-10828
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US-09-949-016-10828
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Search completed: August 30, 2006, 04:33:04 Job time : 15.8485 secs

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Published_Applications Mucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_New databases; older published

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_New). Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_New).

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us-10-758-165a-1.rapbm

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33, Appli
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177658,
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30, Appl
19689, A
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1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US108_PUBCOMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US108_PUBCOMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*
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                                                            (without alignments)
91.717 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1,
                                                   August 30, 2006, 04:33:28 ; Search time 75.7576 Seconds
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Sequence 2
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                                                                                                                                   2097797
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US-10-732-923-17586
                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                2097797 segs, 463214858 residues
                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                 OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                     1 RNDSPIQTDQYTTTG 15
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Maximum DB seq length: 200000000
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Match Length
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No.
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US-IU-/43-40/-4

Sequence 2, Application US/10723207

Publication No. US20050250934A1

GENERAL INFORMAT: Wang, Chang Yi

APPLICANT: Wang, Chang Yi

APPLICANT: Walfield, Alan M.

TITLE OF INVENTION: PEPPINDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF

TITLE OF INVENTION: ALLERGY

FILE REFERENCE: 1151-4153042

CURRENT APPLICATION NUMBER: US/10/723,207

CURRENT APPLICATION NUMBER: US/10/723,207

PRIOR PILING DATE: 2000-12-01

PRIOR PELING DATE: 1999-06-21

PRIOR FILING DATE: 1999-06-21

PRIOR FILING DATE: 1999-06-21

PRIOR FILING DATE: 1998-06-21

PRIOR FILING DATE: 1998-06-21

SRIOR APPLICATION NUMBER: 09/100,287

NUMBER OF SEQ ID NOS: 91

SSQ ID NO 2
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                                Sequence 135296,
Sequence 4, Appli
Sequence 44580, A
Sequence 20346, A
Sequence 61, Appl
Sequence 59, Appl
Sequence 50638, A
Sequence 50638, A
Sequence 260586,
Sequence 26656,
Sequence 26, Appl
                                                                    44580, A
20346, A
20346, A
20437, A
50638, A
50638, A
50638, A
50638, A
260566,
260566,
2645,
26495,
26495, A
117513,
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                                                                                                                                                                                                                                                                                              Squence 1, Application US/10758165
Publication No. US20050196816A1
GENERAL INFORMATION:
APPLICANT: Hammerberg, Bruce
TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
FILE REFERENCE: 5051-661
CURRENT APPLICATION NUMBER: US/10/758,165
CURRENT FILING DATE: 2004-01-16
PRIOR PILING DATE: 2003-01-16
NUMBER OF SEQ ID NOS: 16
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin version 3.2
SEQ ID NO 1
SEQ ID NO 1
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Sequence
Sequence
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                   US-10-425-114-65347
US-10-437-963-135296
US-10-504-048-4
US-10-18-298-20346
US-11-18-298-20346
US-10-193-764-51
US-10-193-764-59
US-10-450-763-50637
US-10-450-763-50656
US-10-450-763-50656
US-10-450-763-50656
US-10-450-763-50656
US-10-450-763-50656
US-10-450-763-50656
US-10-450-763-50656
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US-10-450-763-50656
US-10-437-963-117513
US-10-437-963-117513
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Pred. No. 5.4e-07;
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US-10-759-165-1
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                      Query Match
Best Local Similarity
US-10-723-207-2
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Query Match
Best Local Similarity 57.1<sup>1</sup>
Matches 8; Conservative
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j Publication No. US20330073142A1

j Publication No. US20330073142A1

j GENERAL INFORMATION:
    APPLICANT: Chen, Swey-Shen Alex
    APPLICANT: Warg, Yong-Min
    APPLICANT: Chen, Zhong
    TITLE OF INVENTYON: InfWINVENDLEDBLIN E VACCINES AND METHODS OF USE THEREOF
    TITLE OF INVENTY ON UNMER: US/10/214,524
    CURRENT APPLICATION NUMBER: 60/312,120
    PRIOR APPLICATION NUMBER: 60/312,120
    PRIOR PILLOATION NUMBER: 60/312,120
    PRIOR FILLING DATE: 2001-08-13
    NUMBER OF SEQ ID NOS: 61
    SEQ ID NO 28
    LENGTH: 426
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TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
FILE REFERENCE: 5051-661
CURRENT APPLICATION NUMBER: US/10/758,165
CURRENT FILING DATE: 2004-01-16
PRIOR PELICATION NUMBER: US 60/440,472
PRIOR FILING DATE: 2003-01-16
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                                                                                                                                                                                                                                            100.0%; Score 81; DB 5; Length 312; 100.0%; Pred. No. 1.6e-05;
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                                                                                                                                                                                                                                                                                    0; Indels
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                                                FEATURE:
OTHER INFORMATION: CH2CH3n of dog IgB PUBLICATION INFORMATION:
AUTHORS: Patel,
JOURNAL: Immunogenetics
VOLUME: 41
PAGES: 282-286
DATE: 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 7, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:
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; ORGANISM: Dog (Canis familiaris)
US-10-214-524-28
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; SOFTWARE: Patentin version 3.2
; SEQ ID NO 7
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Sus scrofa
US-10-758-165-7
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Best Local Similarity 100...
Local Similarity 100...
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Matches 15; Conservative
                TYPE: PRT
ORGANISM: Dog
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US-10-758-165-7
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LENGTH: 312
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Sequence 33, Application US/10214524
; Bequence 33, Application No. US20030073142A1
; Bedlication No. US20030073142A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Swey-Shen Alex
; APPLICANT: Barankiewicz, Theresa J.
; APPLICANT: Chen, Zhong
; APPLICANT: Chen, Zhong
; APPLICANT: Chen, Zhong
; APPLICANT: Chen, Zhong
; TITLE REFERENCE: IGE-00101.P.1.1
; CURRENT APPLICATION NUMBER: US/10/214,524
; CURRENT FILING DATE: 2002-08-08
; PRIOR PILING DATE: 2001-08-13
; PRIOR FILING DATE: 2001-08-13
; SEQ ID NOS: 61
; SEQ ID NO 33
; LENGTH: 567
; TERMET 567
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Publication No. US20050196816A1
GENERAL INFORMATION:
APPLICATION NO. US20050196816A1
GENERAL INFORMATION:
ITILE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
FILE REFERENCE: 5051-661
CURRENT APPLICATION NUMBER: US/10/758,165
CURRENT FILING DATE: 2004-01-16
PRIOR PILING DATE: 2003-01-16
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin version 3.2
SEQ ID NO 2.
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Pred. No. 2.1;
5; Mismatches 1; Indels
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Length 15;
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Score 53; DB 5;
Pred. No. 0.039;
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                                     5; Mismatches
  65.4%;
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Best Local Similarity 57.1%;
Matches 8; Conservative
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1 RNDAPVQADRHSTT 14
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Best Local Similarity 61.57
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2 NDSPVRTEQQATT 14
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US-10-214-524-33
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; LENGTH: 496
; TYPE: PRT
; ORGANISM: Felis catus
US-09-479-614-2
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 SEQ ID NO 2
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                                       APPLICANT: McCall, Catherine
APPLICANT: Weber, Eric
TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
FILE REPRENCE: P-10.47
CURRENT PAPLICATION NUMBER: US/09/479,614
CURRENT FILING DATE: 2000-01-07
EARLIER APPLICATION NUMBER: 60/115,033
EARLIER PILING DATE: 1999-01-07
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1.04
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Publication No. US20030013183A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wcdall, Catherine
APPLICANT: Weber, Eric
TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
FILE REFERENCE: P-1047
CURRENT APPLICATION NUMBER: US/09/479,614
CURRENT FILING DATE: 2000-01-07
EARLIER PAPLICATION NUMBER: 60/115,033
EARLIER PAPLICATION OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 2,0
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61.5%; Pred. No. 12;
tive 3; Mismatches 2; Indels
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61.5%; Pred. No. 12;
tive 3; Mismatches 2; Indels
Sequence 14, Application US/09479614
Publication No. US20030013183A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                   363 NDSPVRTEQQATT 375
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                                                                                                                                                                                                                                                                                                                                                                               2 NDSPIQTDQYTTT 14
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Matches 8; Conservative
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Matches 8; Conservative
                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Felis catus
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                                                                                                                                                                                                                                                                               US-09-479-614-14
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Sequence 25, Application US/10214524
; Sequence 25, Application No. US20030073142A1
; GENERAL INFORMATION:
    APPLICANT: Chen, Swey-Shen Alex
; APPLICANT: Tang, Young-Min
; APPLICANT: Chen, Zhong
; APPLICANT: Chen, Zhong
; TITLE OF INVENTION: IMMUNOCLOBULIN E VACCINES AND METHODS OF USE THEREOF
; TITLE OF INVENTION: IMMUNOCLOBULIN E VACCINES AND METHODS OF USE THEREOF
; FILE REFERENCE: IGE-00101.P1.1
; CURRENT APPLICATION NUMBER: US/10/214,524
; CURRENT PILING DATE: 2002-08-08
; PRIOR FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 61
; SEQ ID NO 25
; LENGTH: 496
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Sequence 29. Application No. UG20030013183A1

GENERAL INFORMATION:
APPLICANT: Mocall, Catherine
APPLICANT: Weber, Exic
TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
FILE REFERENCE: P-1047
CURRENT APPLICATION NUMBER: US/09/479,614
CURRENT FILING DATE: 2000-01-07
EARLIER FILING DATE: 1999-01-07
BARLIER PILING DATE: 1999-01-07
SOFTWARE: PATENTING OF SEQ ID NOS: 34
SEQ ID NOS: 34
                                                    Gaps
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Score 48; DB 3; Length 496;
Pred. No. 14;
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Pred. No. 14;
3; Mismatches 2; Indels
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Pred. No. 14;
3; Mismatches
       Query Match
Best Local Similarity 61.5%;
Matches 8; Conservative
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Best Local Similarity 61.5%;
Matches 8; Conservative
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illarity 61.5%;
Conservative
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428 NDSPVRTEQQATT 440
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; ORGANISM: Cat (Felis catus)
US-10-214-524-25
                                                                                                  2 NDSPIOTDOYTTT 14
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, ORGANISM: Felis catus
US-09-479-614-29
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TYPE: PRT ORGANISM: Glycine max
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                                                                                                                 Sequence 2, Application US/10409772

| Sequence 2, Application US/10409772
| Publication No. US20030216565A1
| GRNERAL INFORMATION:
| GRNERAL INFORMATION:
| APPLICANT: McCall, Catherine
| APPLICANT: Weber, Eric
| TITLE OF INVERTION: Feline Immunoglobulin E Molecules and Related Methods
| TITLE OF INVERTION NUMBER: US/10/409,772
| CURRENT FILING DATE: 2003-04-07
| PRIOR APPLICATION NUMBER: US/09/479,614
| PRIOR PRILING DATE: 2000-01-07
| NUMBER OF SEQ ID NOS: 34
| SEQ ID NO 2
| SEQ ID NO 2
| LENGTH: 496
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; Sequence 29, Application US/10409772
; Publication No. US20030216565A1
; GENERAL INFORMATION:
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; CURRENT APPLICATION NUMBER: US/10/409,772
; CURRENT FILING DATE: 2003-04-07
; FRICK APPLICATION NUMBER: US/09/479,614
; PRIOR FILING DATE: 2000-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin Ver. 2.0
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Pred. No. 14;
3; Mismatches 2; Indels
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GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
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ilarity 61.5%;
Conservative
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428 NDSPVRTEQQATT 440
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428 NDSPVRTEQQATT 440
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; ORGANISM: Felis catus
US-10-409-772-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Pelis catus
US-10-409-772-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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US-10-424-599-250413
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                                                                                                          US-10-409-772-2
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TITLE OF INVESTION: Soy Nucleic Acid Molecules and Other Molecules Associated With FITTE OF INVESTION: Plants and uses Thereof for Plant Improvement CURRENT FILISON, SOY No. 25644

FILISON FORTS: 2003-64-28

CURRENT FILISON NOTE: 2003-64-28

COMPANION: COMPANION: COMPANION COMPANION CARLOR SAND NOTE: 2003-64-28

COMPANION: CARLOR SAND NOTE: 2003-64-28

COMPANION: CARLOR SAND NOTE: 2003-64-28

RESULT 15

RESULT 15

COMPANION: CARLOR SAND NOTE: 2003-64-28

RESULT 15

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; TYPE: PRT ; ORGANISM: Staphylococcus epidermidis US-10-282-122A-70437
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Query Match 53.1%; Score 43; DB 4; Length 1633; Best Local Similarity 61.5%; Pred. No. 3.7e+02; Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps

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Search completed: August 30, 2006, 05:13:02 Job time: 75.7576 secs

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Sequence 22888, A
Sequence 55064, A
Sequence 15135, A
Sequence 36321, A
Sequence 103150,
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36320, A
103149,
114388,
36319, A
103148,
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38541, A
41189, A
41668, A
54760, A
105306,
                                                                                                                   August 30, 2006, 04:34:57; Search time 7.72727 Seconds (without alignments) 133.695 Million cell updates/sec
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1. /EMC_Celerra_SIDS3/ptcdata/1/pubpaa/US09_NEW_PUB.pep:*

2. /EMC_Celerra_SIDS3/ptcdata/1/pubpaa/US06_NEW_PUB.pep:*

3. /EMC_Celerra_SIDS3/ptcdata/1/pubpaa/US08_NEW_PUB.pep:*

4. /EMC_Celerra_SIDS3/ptcdata/1/pubpaa/US08_NEW_PUB.pep:*

5. /EMC_Celerra_SIDS3/ptcdata/1/pubpaa/US08_NEW_PUB.pep:*

6. /EMC_Celerra_SIDS3/ptcdata/1/pubpaa/US10_NEW_PUB.pep:*

7. /EMC_Celerra_SIDS3/ptcdata/1/pubpaa/US10_NEW_PUB.pep:*

7. /EMC_Celerra_SIDS3/ptcdata/1/pubpaa/US11_NEW_PUB.pep:*

8. /EMC_Celerra_SIDS3/ptcdata/1/pubpaa/US10_NEW_PUB.pep:*
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Sequence 2
Sequence 3
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-11-340-449-902-55064

US-11-350-449-902-55064

US-11-056-358-36321

US-11-056-358-103150

US-11-056-358-114389

US-11-056-358-103149

US-11-056-358-103149

US-11-056-358-103149

US-11-056-358-103149

US-11-056-358-103149

US-11-056-358-114387

US-10-953-349-38542

US-10-953-349-38542

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                                                                                  OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Sequence 22888, Application US/10953349

RENERAL INFORMATION:
APPLICANT: ALEXANDROW, Nickolai et al.
APPLICANT: ALEXANDROW, Nickolai et al.
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579F035
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 4025-2
SOFTWARE: Patentin version 3.3
SEQ ID NO 22888
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                                              Sequence 95149, A Sequence 91392, A Sequence 91392, A Sequence 9148, A Sequence 11, Appl Sequence 17, Appl Sequence 74126, A Sequence 32, Appl Sequence 8759, Ap Sequence 8759, Ap Sequence 8758, Ap Sequence 8758, Ap Sequence 3346, Ap
                               91393, A
95149, A
78226, A
91392, A
95148, A
74127, A
117, Appl
74126, A
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Publication No. US20060123505A1

GENERAL INFORMATION:

APPLICANT: National Institute of Agrobiological Sciences.

APPLICANT: Bio-oriented Technology Research Advancement Institution.

APPLICANT: The Institute of Physical and Chemical Research.

APPLICANT: Poundation for Advancement of International Science.

TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF

TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF

CURRENT APPLICATION NUMBER: 203-05-29

PRIOR PILING DATE: 2002-05-30

PRIOR PLING DATE: 2002-05-30
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   Sequence
Sequence
Sequence
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US-11-056-355B-78227

US-11-056-355B-95149

US-11-056-355B-95149

US-11-056-355B-95149

US-11-056-355B-91392

US-11-056-355B-91392

US-11-056-355B-74127

US-11-056-355B-74127

US-11-070-573-17

US-11-070-573-17

US-11-056-355B-74125

US-11-056-355B-8759

US-11-056-355B-8759

US-11-174-307B-4644

US-11-174-307B-4644

US-11-056-355B-8759

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US-11-056-355B-8759

US-11-174-307B-4644

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Best Local Similarity 63.00
   5 PIQIDOYTITG 15
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PSQTDRFNTTG 22
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 US-10-953-349-22888
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   TYPE: PRT
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SOFTWARE: Pate SEQ ID NO 55064

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RESULT 5
JS-11-056-355B-103150
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Publication No. US20060150283A1

GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
TITLE OF INVENTION: Polypetides Encoded Thereby
FILE REFERENCE: 2750-1590PUS2
CURRENT FILING DATE: 2005-02-14
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR FILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
SEQ ID NO 36321
LENGTH: 276
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Sequence 15135, Application US/11330403

Sequence 15135, Application US/11330403

Publication No. US2060159563A1

GENERAL HOPRAPHICON:

TITLE OF INVENTION: Genes and Uses for Plant Improvement

FILE REFERENCE: 38-21(53629)B

CURRENT FPLICATION NUMBER: US/11/330,403

UNDER OF SEQ ID NOS: 19250

BEQ ID NO 15135

LENGTH: 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49.4%; Score 40; DB 7; Length 661; 69.2%; Pred. No. 37;
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                                                                                           DB 6; Length 632;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Indels
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                                                                                                                                   2; Indels
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; OTHER INFORMATION: Ceres Seq. ID no. 12321429
US-11-056-355B-36321
                                                                                           Score 40; DB Pred. No. 35; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Bacillus cereus ATCC 14579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: prt
ORGANISM: Arabidopsis thaliana
                                                                                             Query Match
Best Local Similarity 60.0%;
Matches 6; Conservative
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Matches 9; Conservative
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                                                                                                                                                                                            231 NDEPLOTORY 240
                                                                                                                                                                        2 NDSPIQTDQY 11
; LENGTH: 632
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-55064
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183 APVQTDQY 190
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Matches 6; Conserv
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US-11-330-403-15135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                APPLICANT: Brover, Vyacheslav
APPLICANT: Brover, Vyacheslav
APPLICANT: Alexandrov, Nickolai
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENCE: 2750-1590FUS2
CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2005-02-14
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR FILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
SEQ ID NO 103150
LENGTH: 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fragments and Corresponding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 114389, Application US/11056355B
; Publication No. US20660150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments;
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: 08/11/056,355B
; CURRENT APPLICATION NUMBER: 60/544,190
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 114389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48.1%; Score 39; DB 7; 75.0%; Pred. No. 22; tive 2; Mismatches
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; OTHER INFORMATION: Ceres Seq. ID no. 13612112
US-11-056-355B-114389
                                                                                                                                                                                                                                                                                                                                                                                                                    ) LOCATION: (1) ...(276)
) OTHER INFORMATION: Ceres Seq. ID no. 13612112
US-11-056-355B-103150
Sequence 103150, Application US/11056355B Publication No. US20060150283A1 GENERAL INFORMATION:
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; Sequence 36320, Application US/11056355B
; Publication No. US20060150283A1
                                                                                                                                                                                                                                                                                                                                                      TYPE: prt
ORGANISM: Arabidopsis thaliana
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ORGANISM: Arabidopsis thaliana
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Best Local Similarity 75.v-
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Best Local Similarity
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RESULT 10
US-11-056-355B-36319
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           APPLICANT: Brover, Vyacheslav
APPLICANT: Alexandrov, Nickolai
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENCE: 2750-1590FUS2
CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2005-02-14
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR FILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
SEQ ID NO 36320
LENGTH: 294
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APPLICANT: Brover, Vyacheslav
APPLICANT: Alexandrov, Nickolai
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REPERBUCE: 2750-1590PUS2
CURRENT FILING DATE: 2005-02-14
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR PILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
SEQ ID NO 103149
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; Publication No. US20060150283A1
; GRNERAL INFORMATION:
APPLICANT: Brover, Vyacheslav
APPLICANT: ALexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48.1%; Score 39; DB 7; Length 294; 75.0%; Pred. No. 23; tive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                           , LOCATION: (1)..(294)
; OTHER INFORMATION: Ceres Seq. ID no. 12321428
US-11-056-3558-36320

    DOCATION: (1)..(294)
    OTHER INFORMATION: Ceres Seq. ID no. 13612111
    US-11-056-355B-103149

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US-11-056-355B-103149
; Sequence 103149, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                        TYPE: prt
ORGANISM: Arabidopsis thaliana
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ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 75.0
Matches 6; Conservative
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201 APVQTDQY 208
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GENERAL INFORMATION:
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US-11-056-355B-114388
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LOCATION: (1)..(2)
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Matches
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Sequence 36319, Application US/11056355B
; Publication No. US20060150283A1
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypebtides Encoded Thereby
; FILE OF INVENTION: Polypebtides Encoded Thereby
; FILE REFERENCE: 2750-1590FUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT PILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 2005-02-14
; PRIOR APPLICATION NUMBER: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 36319
; LENGTH: 295
; TYPE: prt
CORRANISM: Arabidopsis thaliana
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Sequence 103148, Application US/11056355B

Sequence 103148, Application US/11056355B

PUBLICATION NO. US20060150283A1

GENERAL INFORMATION:

APPLICANT: Brover, Vyacheslav

APPLICANT: Alexandrov, Nickolai

TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding

TITLE OF INVENTION: Polypeptides Encoded Thereby

FILE REFERENCE: 2750-1590PUS2

CURRENT APPLICATION NUMBER: US/11/056,355B

CURRENT FILING DATE: 2005-02-14

PRIOR FILING DATE: 2004-02-13
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Pred. No. 23;
2; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                        | NAME/KEY: peptide
| LOCATION: (1)..(294)
| JOCATION: (1)..(294)
| JUER INDERATION: Ceres Seq. ID no. 13612111
| US-11.056-355B-114388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , LOCATION: (1)...(295)
, OTHER INFORMATION: Ceres Seq. ID no. 12321427
US-11-056-3558-36319
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FILE REFERENCE: 2750-1590PUS2
CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2005-02-14
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR FILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
LENGTH: 294
                                                                                                                                                                                                     TYPE: prt
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                   48.1%;
75.0%;
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Best Local Similarity 75.00,
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Best Local Similarity 75.0.
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201 APVQTDQY 208
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Sequence 38541, Application US/10953349

Publication No. US20060107345A1

GENERAL INFORMATION:

APPLICANT: ALEXANDROW, Nickolai et al.

TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

TITLE OF INVENTION: BROONED THERBY
FILE REFERENCE: 2750-1579FUS2

CURRENT APPLICATION NUMBER: US/10/953,349

CURRENT APPLICATION NUMBER: 2004-09-30

NUMBER OF SEQ ID NOS: 40252

SOFTWARE: Patentin version 3.3
                                                                                                                                                                                                                                            Sequence 3852, Application US/10953349
; Sequence 3852, Application US/10953349
; Sequence 3852, Application No. US20060107345A1
; GENERAL INFORMATION:
    APPLICANT: ALEXANDROW, Nickolai et al.
    TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579FUS2
; CURRENT APPLICATION WINBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patentin version 3.3
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Query Match 46.9%; Score 38; DB 6; Length 211; Best Local Similarity 46.7%; Pred. No. 24; Matches 7; Conservative 2; Mismatches 6; Indels
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46.7%; Pred. No. 35;
tive 2; Mismatches 6; Indels
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46.7%; Pred. No. 47;
tive 2; Mismatches
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Job time : 7.72727 secs
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US-10-953-349-38542
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Best Local Similarity 46.7
Matches 7; Conservative
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Best Local Similarity 46.7
Matches 7; Conservative
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US-10-953-349-38542
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US-10-953-349-38541
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LENGTH: 386
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LENGTH: 294
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Publication No. US20060107345A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRACMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REPRESENCE: 275-01579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 38543
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: BOCKET, Vyacheslav
APPLICANT: Alexandrov, Nickolai
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENCE: 2750-1590PUS2
CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2005-02-14
PRIOR PILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
SEQ ID NO 114387
LENGTH: 295
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; LOCATION: (1)..(295)
; OTHER INFORMATION: Ceres Seq. ID no. 13612110
US-11-056-3558-114387
                                                                                                                                               ; NAME/KEY: peptide
; LOCATION: (1)..(295)
; OTHER INPORMATION: Ceres Seq. ID no. 13612110
US-11-056-355B-103148
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ORGANISM: Zea mays subsp. mays
US-10-953-349-38543
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ORGANISM: Arabidopsis thaliana
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ORGANISM: Arabidopsis thaliana
         NUMBER OF SEQ ID NOS: 119966
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Best Local Similarity 75.0
Matches 6; Conservative
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Best Local Similarity 75.0
Matches 6; Conservative
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US-10-953-349-38543
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LENGTH: 295
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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August 30, 2006, 04:15:52; Search time 54.5455 Seconds (without alignments) 125.735 Million cell updates/sec Run on:

1 HNDSPVRTEQOATTW 15 US-10-758-165A-2 85 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2589679 segs, 457216429 residues Searched:

2589679 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2000s:* geneseqp2001s:* geneseqp2002s:* geneseqp2003bs:* geneseqp2004s:* geneseqp2005s:* geneseqp2003as:* geneseqp1980s:* geneseqp1990s:* A Geneseq 8:* •• Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2006s:*

SUMMARIES

,		مه د			SOPPERATES	
Result No.	Score	Match	Query Match Length	08	ΩI	Description
н	85	0	15	æ	ADR10602	Adr10602 Cat IgE e
7	82	100.0	431	œ	ADG73237	Adg73237 Cat immun
m	85	100.0	496	9	ABP96580	-
4	82	100.0	496	9	ABU09338	Feli
ß	82	100.0	496	9	ABU09336	Abu09336 Feline Ig
9	82	100.0	496	œ	ADG73251	Adg73251 Cat parti
7	82	100.0	496	œ	ADG73225	Cat
80	48	56.5	15	œ	ADR10601	Dog
σ	48	56.5	312	m	AAY79995	
10	48	56.5	417	~	AAW23067	Aaw23067 Canine Ig
11	48	56.5	426	~	AAR97753	Aar97753 Canine Ig
12	48	56.5	426	9	ABP96583	Abp96583 Dog IgE h
13	47	55.3	84	9	ABU55745	-
14	46	54.1	449	4	ABB60974	Abb60974 Drosophil
15	45	52.9	321	4	AAE12007	Aae12007 Streptomy
16	45	52.9	321	9	ABG73760	Abg73760 S. cattle
17	44	51.8	673	4	ABB71738	Abb71738 Drosophil
18	43	50.6	470	œ	ADS27897	
19	43	50.6	969	œ	ADX67175	Adx67175 Plant ful
20	42	49.4	87	4	AAU55966	Aau55966 Propionib
21	42	49.4	87	9	ABM52485	Abm52485 Propionib
22	42	49.4	178	ហ	ABB83494	Abb83494 Human zin
23	42	49.4	178	7	ADB65732	Adb65732 Human pro

Abo60445 Human gen	Ada54799 Human pro	Aao27216 Human zin	Aam79729 Human pro	Aam78745 Human pro	Ady18750 PRO polyp	_	Aau59982 Propionib	Abm56501 Propionib	Aam18098 Peptide #	Abb37133 Peptide #	Aam30608 Peptide #	Abb22444 Protein #	Aam70271 Human bon	Aam57851 Human bra	Aam05733 Peptide #	Aau30476 Novel hum	Aed71188 Corynebac	Aed71186 Corynebac	Aag92695 C glutami	Abg19065 Novel hum	Adp29882 Human sec
ABO60445	ADA54799	AA027216	AAM79729	AAM78745	ADY18750	AAE33775	AAU59982	ABM56501	AAM18098	ABB37133	AAM30608	ABB22444	AAM70271	AAMS 7851	AAM05733	AAU30476	AED71188	AED71186	AAG92695	ABG19065	ADP29882
197 8	296 6	296 7	349 4	430 4	536 9	537 6	70 4	20 6	152 4	152 4	152 4	152 4	152 4	152 4	152 4	349 4	381 9	534 9	647 4	812 4	1194 8
49.4	49.4	49.4	49.4	49.4	49.4	49.4	48.2	48.2	48.2	48.2	48.2	48.2	48.2	48.2	48.2	48.2	48.2	48.2	48.2	48.2	48.2
42	42	42	42	42	42	42	41	41	41	41	41	41	41	41	41	41	41	41	41	41	41
24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

Antiasthmatic; Antiallergic; Immunosuppressive; IgE; dog; asthma; anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody; Cat IgE epitope recognised by monoclonal antibody 5.91, SEQ ID 2. ADR10602 standard; peptide; 15 AA 21-OCT-2004 (first entry) ADR10602; RESULT 1 ADR10602

WO2004065936-A2. Felis catus.

05-AUG-2004.

15-JAN-2004; 2004WO-US003566.

(UYNC-) UNIV NORTH CAROLINA STATE.

16-JAN-2003; 2003US-0440472P.

Hammerberg B;

WPI; 2004-593545/57.

Novel antibody that specifically binds to mammalian IgE epitope, useful for testing an allergen reactivity of IgE sample, detecting mammalian IgE or treating asthma or anaphylactic shock.

Example 6; Page 9; 14pp; English.

The present invention relates to a novel monoclonal antibody (1) that specifically binds to a mammalian IgE epitope, where the epitope is between amino acids 145-166 or 356-374 of mammalian IgE, e.g. dog IgE. (1) is useful for testing an allergen reactivity of an IgE sample. The allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut and corn allergens. The sample is a biological sample collected from a dog, cat or horse. (1) is also useful for detecting mammalian IgE and for treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal antibodies recognise epitopes on canine IgE corresponding to amino acid residues 357-371 (ADR10601) and 146-162 (ADR10609) respectively of the

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention describes an isolated nucleic acid molecule (I) encoding a portion of a feline IgE heavy chain protein. The methods and compositions of the present invention are useful for eliciting feline immune responses for and/or treating IGE-mediated responses, such as allergies. This is the amino acid sequence of a cat immunoglobulin E (IgE) constant region.
canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and 3.76 ware observed to have good cross-reactivity with the epsilon-chain of IgE from cat and horse, but did not exhibit cross-reactivity with either pig or human epsilon-chains of IGE. The present sequence is the cat IGE 5.91 recognition site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated nucleic acid molecule encoding a portion of a feline IgB heavy chain protein, useful for treating and/or eliciting feline immune responses for IGE-mediated responses, such as allergies.
                                                                                                                                                                                                                                                                                       antiallergic; IgE-modulator; vaccine; feline; IgE; immunoglobulin E; immune response; IgE-mediated response; allergy; cat; constant region.
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                                                                                              DB 8; Length 15;
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**A 0%; Pred. NO. 6e-08;
Tropes 0; Indels
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100.0%; Pred. No. 2.6e-06;
ive 0; Mismatches 0;
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                                                                                                                                                                                                          ADG73237 standard; protein; 431 AA.
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                                                                                                                  15; Conservative
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                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 431 AA;
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                                                                          Sequence 15 AA;
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The present invention describes a method (M1) for identifying peptides that induce cytotoxic T-lymphocyte (CTL) response against immunoglobulin (CC E (IgE), comprising providing a test peptide (TT) suspected of being able to bind to major histocompatibility complex (MHC) class I molecule, and evaluating (T) for ability to elicit in a mammal a CTL response to naturally processed and presented IgE peptides, where a peptide that induces such a response is identified. Also described are compositions: (CI) comprising at least one immunogenic peptide (I) identified by (M1); (CC) comprising at least one isolated polynucleotide encoding (I); and (CC) comprising at least one isolated polynucleotide encoding (I); and (CC) comprising at least one isolated polynucleotide encoding (I); and (CC) comprising at least one isolated polynucleotide encoding (I); and (CC) comprising at least one isolated polynucleotide encoding (I); and (CC) are able to bind to at least one MHC class I molecule and to elicit in a mammal a CTL response to naturally processed and presented (CC) elicit in a mammal a CTL response to naturally processed and presented (CC) and can be used as inducers of a CTL response against IgE, and in a composition such as an encountered atopic hypersensitivity condition, IgE-mediated condition in a companient of the presential condition, IgE myeloma in a mammal. Preferably, Cl-3 are useful for treating atopic hypersensitivity conditions (such as allergic ribinitis, allergic asthma, food allergies, or atopic dermatitis), nonthic atopic hypersensitivity conditions (such as allergic at the present seminary perpensions and an applylants, and and a condition and an adaphylants, and an encounted perpension and ada
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                                                                                                                                                                                                                                                                                                                                                                                                                     Immunoglobulin B; vaccine; IgE; cytotoxic T lymphocyte response; immune response; major histocompatibility complex; MHC; immunogenic; antiallergic; antiasthmatic; immunosuppressive; vasotropic; cytostatic; dermatological; antiinflammatory; IgE-mediated condition; food allergy; atopic hypersensitivity condition; allergic rhinitis, allergic asthma; atopic dermatits; non-atopic hypersensitivity onaphylaxis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hives). The present sequence represents an IgE heavy chain amino acid sequence, which is given in an example from the present invention
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                                                                                                                                                                                                                                                                                                                    Cat IgE heavy chain amino acid sequence SEQ ID NO:25.
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100.0%; Pred. No. 3e-06;
Micmatches 0;
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ABP96580 standard; protein; 496 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-AUG-2002; 2002WO-US026986.
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New nucleic acid molecule encoding feline immunoglobulin E (IgE) heavy or light chain protein, useful for treating feline IgE-mediated responses e.g. allergies, parasitic infections or neoplasia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (IgB) kappa light chain and IgB epsilon heavy chain proteins, and the polymuclectide sequences encoding them. The sequences of the invention are useful for treating feline IgB-mediated immune responses (e.g. allergies, parasitic infections or neoplasia), in vaccine technology, small moleculefantibody technology, molecular biology, and various immunological techniques related to feline IgB and its functions. The present sequence represents feline IgB epsilon heavy chain #1
     IgE-mediated immune response; allergy; neoplasia; vaccine technology; antibody technology; antiallergic; antiparasitic; cytostatic.
                                                                                                    /note= "This sequence is given as SEQ ID No:14 and is specifically claimed in Claim 12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antiallergic; IgE-modulator; vaccine; feline; IgE; immunoglobulin E;
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                                                                                                                                               SEQ ID
                                                                                                                                                                                        sequence is given as SEQ ID claimed in Claim 10"
                                                                                                                                               /note= "This sequence is given as specifically claimed in Claim 9"
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specifically claimed in Claim 11"
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                                                                          location/Qualifiers
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/note= "This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-391997/37.
N-PSDB; ABX95713.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Mccall C, Weber E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                              (MCCA/) MCCALL C.
                                                                                                                                                                                                                                                                                                                                                                                                           (WEBE/) WEBER E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 496 AA;
                                                                                                                                                                                                                                                                             JS2003013183-A1
                                                                                                                                                                                                                                                                                                                                                                 07-JAN-1999;
                                            Felis catus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cat partial
                                                                                                                                                                                                                                                                                                          16-JAN-2003
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                                                                            Key
Region
                                                                                                                                  Region
                                                                                                                                                                            Region
                                                                                                                                                                                                                      Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to the isolation of feline immunoglobulin E (IgB) kappa light chain and IgB epsilon heavy chain proteins, and the polynucleotide sequences encoding them. The sequences of the invention are useful for treating feline IgB-mediated immune responses (e.g. allergies, parasitic infections or neoplasia), in vaccine technology, anleucule antibody technology, molecular biology, and various immunological techniques related to feline IgB and its functions. The present sequence represents feline IgB epsilon heavy chain #2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or
                                                                                                                                                                                                 Feline, immunoglobulin E; IgE epsilon heavy chain; parasitic infection; IgE-mediated immune response; allergy; neoplasia; vaccine technology; antibody technology; antiallergic; antiparasitic; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Feline; immunoglobulin E; IgE epsilon heavy chain; parasitic infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid molecule encoding feline immunoglobulin E (IgE) heavy light chain protein, useful for treating feline IgE-mediated responses e.g. allergies, parasitic infections or neoplasia.
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100.0%; Pred. No. 3e-06;
                                                                                     ABU09338 standard; protein; 496 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABU09336 standard; protein; 496 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 37-39; 45pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Feline IgE epsilon heavy chain #1.
                                                                                                                                                                       Feline IgE epsilon heavy chain #2.
                                                                                                                                                                                                                                                                                                                                                  07-JAN-2000; 2000US-00479614
                                                                                                                                                                                                                                                                                                                                                                             99US-0115033P
                   441
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Best Local Similarity 100....
Best Act 15; Conservative
                                                                                                                                            (first entry)
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WPI; 2003-391997/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Weber E;
                                                                                                                                                                                                                                                                                                                                                                                                          MCCALL C.
WEBER E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; ABX95715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 496 AA;
                                                                                                                                                                                                                                                                                        US2003013183-A1
                                                                                                                                                                                                                                                                                                                                                                          07-JAN-1999;
                                                                                                                                            27-JUN-2003
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                                                                                                                                                                                                                                                                                                                      16-JAN-2003.
                                                                                                                                                                                                                                                             Felis catus
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mccall C,
                427
                                                                                                                 ABU09338
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(WEBE/)
                                                                    ABU09336
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Gaps

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WPI; 2004-010802/01
           N-PSDB; ADG73224
                                                                                                                                                                          Sequence 496 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hammerberg B;
                                                                                                                                                                                                                                                                                                                                                             21-OCT-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-AUG-2004
                                                                                                                                                                                                                                                                                                                                          ADR10601;
                                                                                                                                                                                                                                                               427
                                                                                                                                                       chain.
                                                                                                                                                                                                                                                                                                           ADR1060
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                                                                                                                                                                                                                                                                                  The invention describes an isolated nucleic acid molecule (I) encoding a portion of a feline IgE heavy chain protein. The methods and compositions of the present invention are useful for eliciting feline immune responses for and/or treating IGE-mediated responses, such as allergies. This is the amino acid sequence of a partial cat immunoglobulin E (IgE) heavy
                                                                                                                                                                                                                     New isolated nucleic acid molecule encoding a portion of a feline IgE heavy chain protein, useful for treating and/or eliciting feline immune responses for IGE-mediated responses, such as allergies.
                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antiallergic; IgE-modulator; vaccine; feline; IgE; immunoglobulin E; immune response; IgE-mediated response; allergy; cat; heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 85; DB 8; Length 496; 100.0%; Pred. No. 3e-06; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cat partial immunoglobulin E (IgE) heavy chain #1.
                                                                                                                                                                                                                                                                Claim 8; SEQ ID NO 29; 44pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADG73225 standard; protein; 496 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-JAN-1999; 99US-0115033P.
07-JAN-2000; 2000US-00479614.
                                                                                               07-JAN-1999; 99US-0115033P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-APR-2003; 2003US-00409772
                                                                            07-APR-2003; 2003US-00409772
                                                                                                                                                                                                                                                                                                                                                                                                                                                     441
                                                                                                                                                                                                                                                                                                                                                                                                                                1 HNDSPVRTEQOATTW 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                            427 HNDSPVRTEQQATTW
                                                                                                                                                                                                                                                                                                                                                                                                           15; Conservative
                                                                                                                                                                                      WPI; 2004-010802/01.
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Best Local Similarity
                                                                                                                                                                 Accall C, Weber E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MCCA/) MCCALL C. (WEBE/) WEBER E.
                                                                                                                               (MCCA/) MCCALL C. (WEBE/) WEBER E.
                                                                                                                                                                                                 N-PSDB; ADG73250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US2003216565-A1.
                                                                                                                                                                                                                                                                                                                                                                 Sequence 496 AA;
                                 US2003216565-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Felis catus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-NOV-2003
             Felis catus
                                                     20-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Mccall C, Weber E;

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                                                                                                                                      The invention describes an isolated nucleic acid molecule (I) encoding a portion of a feline IgE heavy chain protein. The methods and compositions of the present invention are useful for eliciting feline immune responses for and/or treating IGE-mediated responses, such as allergies. This is the amino acid sequence of a partial cat immunoglobulin E (IgE) heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel antibody that specifically binds to mammalian IgE epitope, useful for testing an allergen reactivity of IgE sample, detecting mammalian IgE or treating asthma or anaphylactic shock.
New isolated nucleic acid molecule encoding a portion of a feline IgE heavy chain protein, useful for treating and/or eliciting feline immune responses for IGE-mediated responses, such as allergies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antiasthmatic; Antiallergic; Immunosuppressive; IgE; dog; asthma; anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody.
                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dog IgE epitope recognised by monoclonal antibody 5.91, SEQ ID 1.
                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 85; DB 8; Length 496; 100.0%; Pred. No. 3e-06;
                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                 Claim 8; SEQ ID NO 2; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADR10601 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYNC-) UNIV NORTH CAROLINA STATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 6; Page 9; 14pp; English
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-JAN-2003; 2003US-0440472P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HNDSPVRTEQOATTW 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 HNDSPVRTEQQATTW 15
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                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 15; Conserv
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Pred. No. 7.4; 3; Mismatches

61.5%;

Local Similarity

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                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           maximize cross-reactivity to the natural target. They induce safe (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino acid sequences used in the exemplification of the present invention
cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and 3.76 were observed to have good cross-reactivity with the epsilon-chain of IgE from cat and horse, but did not exhibit cross-reactivity with either pig or human epsilon-chains of IgE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen; immunoglobenic; immunostimulatory; carrier protein; helper T cell epitope; antibody; allergy; allergic disease; immunisation; anti-allergic; anti-asthmatic; asthma; anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antigenic peptide from the CH3 domain of immunoglobulin E, fusions immunization against allergy.
                                                                                                                                                                           Gaps
                                                                                                                                                                           ö
                                                                                                                                      Score 48; DB 8; Length 15;
Pred. No. 0.24;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             immunoglobulin E epsilon heavy chain SEQ ID NO:2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 66-68; 155pp; English.
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                                                                                                                                                                                                                                                                                                                                              AAY79995 standard; protein; 312
                                                                                                                                                                           3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98US-00100287,
                                                                                                                                    56.5%;
ilarity 61.5%;
Conservative
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|NDSPIQTDQYTTT 14
                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                2 NDSPVRTEQOATT 14
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                                                                                                                  Query Match
Best Local Similarity
Local 8; Conserve
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                                                                                                     Sequence 15 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W09967293-A1
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                                                                                                                                                                                                                                                                                                                                                                                   AAY79995;
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56.5%; Score 48; DB 3; Length 312;

Query Match

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This polypeptide is encoded by exons 1-4 (see AAT79278) of canine IgE heavy chalan constant region (epsilon) genomic DNA. Another polypeptide, comprising the exon 5 and 6 product, is given in AAW23068 Recombinant peptides encoded by exons 1-6 can be produced in eukaryotic or profused in peptides, and antibodies raised against them, are used in methods to treat the manifestation of allergy in dogs, e.g. to treat Type I immediate hypersensitivity, and for immunomodulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated canine IgE heavy chain constant region DNA - useful to develop products for treatment of canine allergies and for immunomodulation in
                                                                                                                                                                                                                 IgE, immunoglobulin, antibody; heavy chain constant region, allergy; hypersensitivity; therapy; dog; antisense; immunomodulation.
                                                                                                                                                                                          Canine IgE heavy chain constant region (exon 1-4 product).
                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "encoded by GGN"
                                                                                                                                                                                                                                                                                                                                                                                                                                             NNG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "encoded by TGN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "encoded by TCC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "encoded by GAC"
                                                                                                                                                                                                                                                                                                             'note= "encoded by ACC"
                                                                                                                                                                                                                                                                                                                                                               'note= "encoded by GCC"
                                                                                                                                                                                                                                                                                                                                                                                          'note= "encoded by NNT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 35-39; 59pp; English.
                                                                                                                                                                                                                                                                                Location/Qualifiers
55
                                                                                                                                                                                                                                                                                                                                                                                                                                            'note= "encoded by
                                                                                       AAW23067 standard; protein; 417 AA.
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                                                                                                                                                                                                                                                                                                                                        /note= "encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97WO-US002322.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96US-00601197
                |||||::|:|
256 NDSPIQTDQYTTT 268
                                                                                                                                                                   (first entry)
14
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 2 NDSPVRTEQQATT
                                                                                                                                         (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (IDEX-) IDEXX LAB INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mermer B, Harris RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1997-425031/39.
                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference 174
                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference 204
                                                                                                                                                                                                                                                                                                                          Misc-difference 56
                                                                                                                                                                                                                                                                                                                                                                              Misc-difference 83
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                                                                                                                                                                                                                                                           Canis familiaris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAT79278
                                                                                                                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
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                                                                                                                                        30-JUN-2005
16-JUN-2005
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                                                                                                                                                                  19-FEB-1998
                                                                                                                AAW23067;
                                                              RESULT 10
                                                                           AAW23067
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chain amino acid sequence SEQ ID NO:28.

(first entry)

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Identifying peptides that induce cytotoxic T-lymphocyte, CTL response against IgE, by identifying peptide eliciting CTL response to IgE peptides naturally presented by major histocompatibility complex class I
                                                                       Immunoglobulin B; vaccine; IgE; cytotoxic T lymphocyte response; immuno response; major histocompatibility complex; MHC; immunogenic; antiallergic; antiaefhmatic; immunosuppressive; vasotropic; cytostatic; dermatological; antiinflammatory; IgE-mediated condition; food allergy; atopic hypersensitivity condition; allergic rhinitis; allergic asthma; atopic dermatitis; non-atopic hypersensitivity condition; anaphylaxis;
                                                                                                                                                                                                                                                                                                                                                                                                 Example 7; Page 152-154; 187pp; English.
                                                                                                                                                                                                                                08-AUG-2002; 2002WO-US026986.
                                                                                                                                                                                                                                                      L3-AUG-2001; 2001US-0312120P.
                                                                                                                                                                                                                                                                             (IGET-) IGE THERAPEUTICS INC.
                                                                                                                                                                                                                                                                                                                      WPI; 2003-268242/26.
                                                                                                                                                                                                                                                                                                  Yang Y,
                                                                                                                                                               Canis familiaris.
                                                                                                                                            urticaria hives.
                                                                                                                                                                                     WO2003015716-A2
                                                    Dog IgE heavy
                               28-MAY-2003
           ABP96583;
                                                                                                                                                                                                                                                                                                  Chen SA,
                                                                                                                                                                                                                                                                                                                                                                               protein.
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The canine IgE amino acid sequence (AAR97753) was deduced from an isolated gene (AAR29824) obtd. from a canine liver DNA library. The cloning of the IgE gene allows produ. of large quantities of recombinant IgE using bacterial, yeast, mammalian, insect or vixal systems. The IgE can be used in drug development (e.g. small molecule screening, assay development and anti-IgE antibody generation). Fragments of IgE can be used in vaccines or to prevent IgS-mediated hypersensitivity. The new sequence information permits targeted modulation of IgE-mediated immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New DNA encoding canine IgE and IgA - useful in vaccines, anti-sense therapy, assays, drug screening, etc.
                                                                             Gaps
                                                                                                                                                                                                                                                                  IgE; immunoglobulin; antibody; vaccine; allergy; hypersensitivity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 426;
                                                      Length 417;
                                                                           2; Indels
           Revised record issued on 30-JUN-2005 : Typo in comments
                                                       ;
;
                                                      DB
10;
                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 48;
Pred. No.
                                                       Score 48;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 11; Page 29-30; 49pp; English.
                                                                                                                                                                           AAR97753 standard; protein; 426 AA
                                                                         3;
                                                                                                                                                                                                                                                                                                                                                         95WO-US013795
                                                                                                                                                                                                                                                                                                                                                                            94US-00336583.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56.5%;
61.5%;
                                                       56.5%;
                                                                                                              353 NDSPIQTDQYTTT 365
                                                                                                                                                                                                                       (first entry)
                                                                                                2 NDSPVRTEQQATT 14
                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              (MERI ) MERCK & CO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Hollis GF, Patel MD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1996-277321/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAT29824.
                                                                                                                                                                                                                                                                                        Canis familiaris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 426 AA;
                                 Sequence 417 AA;
                                                                                                                                                                                                                                                                                                                                                        03-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                               09-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                         09-NOV-1994;
                                                                                                                                                                                                                                                                                                              WO9614867-A1
                                                                                                                                                                                                                       28-AUG-1996
                                                                                                                                                                                                                                                                                                                                   23-MAY-1996
                                                                                                                                                                                                                                              Canine IgE
                                                                                                                                                                                                  AAR97753;
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Chen Z;

Barankiewicz T,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       where C1:3 are and an CTL response to naturally processed and presented 1gE peptides. C1-3 have antiallergic, antiasthmatic, immunosuppressive, vasocropic, dermatological, antialifammaerory and cytostatic activities, and can be used as inducers of a CTL response against 1gE, and in vaccines. C1-3 can be used for modulating an IgE-mediated condition in a mammal. C1-3 are useful for modulating an IgE-mediated condition such as IgE-mediated atopic hypersensitivity condition, IgE-mediated non-atopic hypersensitivity condition, IgE-mediated non-atopic hypersensitivity conditions (such as allergic rathma, food allergies, or atopic dermatitis), non-atopic hypersensitivity conditions (such as allergic sathma, food allergies, or atopic dermatitis), non-atopic hypersensitivity conditions (such as anaphylaxis, and urticaria hives). The present sequence respresents an IgE heavy chain amino acid sequence, which is given in an example from the present invention
The present invention describes a method (M1) for identifying peptides that induce cytotoxic T-lymphocyte (CTL) response against immunoglobulin E (IgE), comprising providing a test peptide (T) suspected of being able to bind to major histocompatibility complex (MHC) class I molecule, and naturally processed and presented IgE peptides, where a peptide that induces such a response is identified. Also described are compositions: (C1) comprising at least one immunogenic peptide (I) identified by (M1); (C2) comprising at least one isolated polynucleotide encoding (I); and (C3) comprising antigen-presenting cells that recognise at least one isolated polynucleotide and compositions: (C3) camprising antigen-presenting cells that recognise at least one (I); where C1-3 are able to bind to at least one MHC class I molecule and to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Length 426;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 48; DB 6
Pred. No. 11;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 NDSPVRTEQOATT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 426 AA;
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Gaps

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2; Indels

Mismatches

RESULT 12 ABP96583 ID ABP96583 standard; protęin; 426 AA.

358 NDSPIQTDQYTTT 370

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2 NDSPVRTEQOATT 14

Conservative

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ss; plant; growth regulating protein; PSK; phytosulphokine-alpha;
transgenic; marker-assisted breeding; agriculture; horticulture.
                                                                                                                                                   Mironov V, Frankard V, Dillen W;
                                            Tree cotton growth regulating protein, GaGREPI.
          ABU55745 standard; protein; 84 AA
                                                                                                                                                                                                                 Claim 5; Fig 22; 156pp; English.
                                                                                                           11-APR-2002; 2002WO-EP004035.
                                                                                                                      12-APR-2001; 2001US-0283313P.
                                (first entry)
                                                                                                                                             Lorbiecke R, P
                                                                                                                                  CROPDESIGN NV
                                                                                                                                                                    WPI: 2003-093023/08
                                                                         Gossypium arboreum.
                                                                                                                                        SAUTER M.
                                                                                                                                                                           N-PSDB; ABX74222
                                                                                    WO200283901-A2.
                                                                                                                                                                                                       tissue culture.
                                17-MAR-2003
                                                                                               24-OCT-2002
                                                                                                                                                        Lejeune P,
                                                                                                                                                   Sauter M,
                     ABUS5745;
                                                                                                                                  (CROP-)
                                                                                                                                        (SAUT/)
RESULT 13
      ABU55745
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growth characteristics of a plant, useful for a wide application in icultural and horticultural practices, and in vitro plant cell and New isolated GREP nucleic acids and polypeptides controlling

The invention relates to a new isolated mucleic acid encoding a growth regulating protein (GREP), where the protein conforms to the GREP regulating protein (GREP), where the protein conforms to the GREP conclains. Also included are a vector comprising a RREP mucleic acid, or a vector alpha) where the growth regulating polypeptide OsPSK (phytosulphokinedalpha) where the growth regulating polypeptide OsPSK (phytosulphokinedalpha) where the growth regulating proteins regulate growth and/or alpha plant comprising the vector, seed/pollen and a harvestable part of propagation material from the transgenic plant, a host cell on unclectides transgenic nation anti-GREP anti-Ody which specifically comprising the GREP nucleic acid, an anti-GREP sequence appearing as AREA 197, an anti-GREP sequence molecule consisting of 14.

To nuclectides transgenic to the GREP signature nuclectide sequence appearing as AREA 197, an anti-GREP anti-Ody which specifically recognises a GREP or is fragment, a method for altering growth and/or activity of a plant cell/storage organ comprising modulating the recognises a GREP or its activity of a GREP or the rice growth regulating peptide osps. is an enthod for downregulating levels of a GREP or Osps. or organs or deatures which comprises isolating alleles for a GREP or osps. or organs or deatures which comprises isolating alleles for a GREP or organs and electing an allele with desired features which comprises isolating alleles for a GREP or osps. organs or organs or deatures. Or organs or organs or organs or deatures. Or organs or organs or organs or organs or deatures. Or organs or organs or organs or organs or deatures which comprises isolating alleles fo

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AAE12007 standard; protein; 321 AA.
RESULT 15
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Sequence 84 AA;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell:cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL1016-ABL30511), expressed DNA sequences (ABL01840-ABL6175) and the encoded proteins (ABB7737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                      Drosophila; developmental biology; cell signalling; insecticide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 9714; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54.1%; Score 46; DB 4; Length 449; 53.3%; Pred. No. 25;
              84;
                                           3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
              Length
                                                                                                                                                                                                                                                         Drosophila melanogaster polypeptide SEQ ID NO 9714.
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                9
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2; Mismatches
                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Myers EW;
              Score 47;
Pred. No.
                                                                                                                                                                     ABB60974 standard; protein; 449 AA.
                                           2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Li PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150
                                                                                                                                                                                                                                                                                                                                                                                                                     23-MAR-2001; 2001WO-US009231.
             55.3%;
ilarity 61.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            133 HNDGFVRCPEEALTW 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 HNDSPVRTEQQATTW 15
                                                                                                                                                                                                                             26-MAR-2002 (first entry)
                                                                    2 NDSPVRTEQOATT 14
                                                                                                 44
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                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster.
                                                                                               NDSPAKTQSQGTT
Query Match
Best Local Similarity
'-hag 8; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-656860/75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; ABL05077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 449 AA;
                                                                                                                                                                                                                                                                                                                                                            WO200171042-A2
                                                                                                                                                                                                                                                                                                     pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         interactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8;
                                                                                                                                                                                                                                                                                                                                                                                        27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Venter JC,
                                                                                                                                                                                                  ABB60974;
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The invention relates to a modified enzyme of a non-haeme iron (II) dependent family of oxygenases and oxidases which renders the enzyme dependent on bicarbonate for activity. The invention also related to a method for producing penicillin G or V comprises employing a modified enzyme, particularly isopenicillin N synthethase (IPNS), in either an organism or a cell-free system, under the control of bicarbonate. The modified enzymes are IPNS, deacetoxycephalosporin C synthetase (DACS) and deacetylcephalosporin C synthetase (DACS). The method is useful for producing antibiotics, particularly penicillin G or V. The method is useful for making organisms useful for making an antibiotic dependent on bicarbonate to make the antibiotic. The present sequence is Streptomyces cattleya modified isopenicillin N synthetase showing an Arg211 in place of Glu211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Method for producing antibiotics, particularly penicillin G or V, comprises employing a modified isopenicillin N synthethase, in either an organism or a cell-free system under the control of bicarbonate.
                                                                                                  Isopenicillin N synthetase; IPNS; antibiotic; penicillin; oxygenase; non-haeme iron (II) dependent family; oxidase; mutant; mutein.
                                                                  Streptomyces cattleya modified isopenicillin N synthetase (IPNS).
                                                                                                                                                                                                                                             /note= "Wild type Glu substituted with Arg"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52.9%; Score 45; DB 4; Length 321; 50.0%; Pred. No. 26; cive 4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Warner TM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wang Z,
                                                                                                                                                                                                    ney Location/Qualifiers
Misc-difference 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 2; Col 37-38; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                         99US-00413231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dilley DR, Kadyrzhanova DK,
                                                                                                                                                                                                                                                                                                                                                                                          99US-00413231
                                                                                                                                                                                                                                                                                                                                                                                                                              (UNMS ) UNIV MICHIGAN STATE
                                 (first entry)
                                                                                                                                                          Streptomyces cattleya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-615433/71.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 321 AA;
                                                                                                                                                                                                                                                                                                                                                         06-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                            06-OCT-1999;
                                 18-DEC-2001
                                                                                                                                                                                                                                                                                  US6284483-B1
                                                                                                                                                                                                                                                                                                                      04-SEP-2001.
                                                                                                                                                                            Synthetic
 AAE12007;
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2 NDSPVRTEQOATTW 15 |:| |:| |:||| NESTTMTDQRSTTW 74 Query Match 52.9 Best Local Similarity 50.0 Matches 7; Conservative ò g

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Gaps

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Search completed: August 30, 2006, 04:22:04 Job time : 56.5455 secs

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GenCore version 5.1.9 (c) 1993 - 2006 Biocceleration Ltd.
                    Copyright
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OM protein - protein search, using sw model

Seconds August 30, 2006, 04:29:42; Search time 8.93939 Run on:

(without alignments) 161.448 Million cell updates/sec

US-10-758-165A-2 Perfect score:

1 HNDSPVRTEQQATTW 15 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched: Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Dirl: *
Dir3: * PIR_80:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote probable exported pol polyp integral glucosyltransferas ExoW protein - Rhi hypothetical prote gag protein - maiz glutamyl-tRNA synt hypothetical prote succinoglycan bios probable RNA-direc methyl-accepting c prote probable seed matu hipB protein - Esc T-cell receptor de T-cell receptor de T-cell receptor de T-cell receptor de int protein - phag multidrug resistan D-galactose-bindin glucosamine-6-phos isopenicillin N sy conserved hypothet probable pol probable inte hypothetical Description SUMMARIES S58484 D87485 AF2006 E49348 A95976 S40175 B85066 T20181 T20180 C31769 C82971 S04917 S04934 AE0204 DB Query Match Length 101 259 1449 1584 1586 151 270 275 410 513 557 631 635 Score Result No.

semaphorin III - m	semaphorin III pre	collapsin - chicke	semaphorin D - mou	gene 16 protein -	cytochrome P450 10	Opaque-2 protein -	regulatory protein	glucuronosyltransf	glucuronosyltransf	glucuronosyltransf	methyl-accepting c	methyl-accepting c	methyl-accepting c	serine chemorecept	methyl-accepting c
158169	D49423	A49069	148747	T03313	O4BS6M	A34800	806022	S15089	JN0619	A42233	QRECM2	C90953	G85801	QRECS	C91293
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999	771	772	772	393	410	437	460	527	528	529	533	533	533	551	554
45.9	45.9	45.9	45.9	44.7	44.7	44.7	44.7	44.7	44.7	44.7	44.7	44.7	44.7	44.7	44.7
39	39	39	39	38	38	38	38	38	38	38	38	38	38	38	38

ALIGNMENTS

RESULT 1
A58458
isopenicillin N synthase (EC 1.14.11) [similarity] - Streptomyces cattleya
C;Species: Streptomyces.cattleya
C; Date: 30-Sep-1993 #sequence revision 21-Jan-1997 #text change 09-Jul-2004
 C;Accession: AS8458
R;Wang, Y.G.; Li, R.F.
Acta Microbiol. Sin. 36, 87-92, 1996
A; Title: Cloning and sequencing the isopenicillin N synthetase (IPNS) gene from Streptom
A;Reference number: A58458
A; Accession: A58458
A;Molecule type: DNA
A; Residues: 1-321 <wan></wan>
A; Cross-references: UNIPROT: Q53932; UNIPARC: UP1000012D7FD
C; Superfamily: isopenicillin N synthase
C;Keywords: antibiotic biosynthesis; ascorbic acid; iron; metalloprotein; oxidoreductase
F,49,213,269/Binding site: iron (His) #status predicted

Gaps .. 0 Length 321; 3; Indels DB 2; 4; Mismatches Score 45; Pred. No. 52.9%; Conservative Query Match Best Local Similarity Matches 7; Conserv

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NDSPVRTEQOATTW 15 61 NESTIMIDORSTIW 74 a ઠ

RESULT 2

D-galactose-binding periplasmic protein mglB-2 - syphilis spirochete
N;Alternate names: carbohydrate receptor; methylgalactoside transport galactose-binding
C;Species Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Date: 16-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 09-Jul-2004
C;Accession: JC5171; D71295
R;Porcella, S.F.; Popova, T.G.; Hagman, K.E.; Penn, C.W.; Radolf, J.D.; Norgard, M.V.
Gene 177, 115-121, 1996
A;Title: A mgl-like operon:in Treponema pallidum, the syphilis spirochete.
A;Reference number: JC5170; MUID:97080510; PMID:8921855

A;Accession: JC5171
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-403 cPOR>
A;Cross-references: UNIPROT:Q08255; UNIPARC:UPI000012F062; GB:U48416; NID:g1230600; PIDN
A;Cross-references: UNIPROT:Q08255; UNIPARC:UPI000012F062; GB:U48416; NID:g1230600; PIDN
B;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDothey, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998

A,Tille: Complete genome sequence of Treponema pallidum, the syphilis spirochete. A,Reference number: A71250; MUID:98332770; PMID:9665876
A,Accession: D71295
A,Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA

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C;Accession: AF2006
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             succinoglycan biosynthesis glycosyltransferase (EC 2.4.1.-) exow [validated] - Rhizobium C;Species: Rhizobium meliloti
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glucosyltransferase protein (EC 2.4.1.-) [imported] - Sinorhizobium meliloti (strain 102 C;Species: Sinorhizobium meliloti
C;Species: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C;Accession: A95976
R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Cross-references: UNIPROT:QRYWK9; UNIPARC:UPI00000CE143; GB:BA000019; PIDN:BAB77970.1; A,Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-283 <CGUJV
A, Cross-references: UNIPROT: P33702, UNIPARC:UP1000016FEBF; GB:L20758; NID:9393240; PIDN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Accession: £49348
R;Glucksmann, M.A.; Reuber, T.L.; Walker, G.C.
J. Bacteriol. 175, 7033-7044, 1993
A;Title: Family of glycosyl transferases needed for the synthesis of succinoglycan by J;Accession: E49348; MUID:94042869; PMID:8226645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Description: BC 2.4.1.-; succinoglycan biosynthesis glycosyltransferase [validated, exoU, and exoW together are responsible for sugar addition to the lipid carrier A; Pathway: succinoglycan biosynthesis C; Keywords: glycosyltransferase; hexosyltransferase
                                                                                                                     hypothetical protein alr1604 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec_2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
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Best Local Similarity 57.1%; Pred. No. 10;
Matches 8; Conservative 1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49.4%; Score 42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 HNDSPVRTEQQATTW 15
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Best Local Similarity
Matches 5; Conserv
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A, Molecule type: DNA
A, Residues: 1-247 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: AF2006
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Genetics:
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A95976
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C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: D87485
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B; Laub, M.T.; DeBson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: D87485
A;Accession: D87485
A;Accession: preliminary
A;Molecule type: DNA
A;Residues: 1-470 <STO>
A;Cross-references: UNIPROT:Q9A721; UNIPARC:UPI00000C7547; GB:AE005673; NID:g13423356; F
C;Genetics:
A;Genetics:
A;Genetics:
A;Genetics: C1905
C;Superfamily: glutamate-tRNA ligase; glutamine-tRNA ligase homology
                                                                                                                                   C;Genetics:
A;Gene: mg1B; TP0684
C;Kepne: mg1B; TP0684
C;Kepne: mg1B; Chemotaxis; periplasmic space; sugar transport
C;Keplwids: calcium binding; chemotaxis; periplasmic space; sugar transport
F;44,114,116,120,197,220/Binding site: galactose (Asn, His, Asp, Arg, Asn, Asp) #status
F;96,98,100,102,104,191/Binding site: calcium (Asp, Asn, Asp, Ile, Gly, Asp) #status pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1-375 «HUM»
A;Cross-references: UNIPARC:UP1000011DE94; EMBL:U11059; NID:g507844; PIDN:AAA91147.1; PI
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1994
                        A;Cross-references: UNIPARC:UP1000012F062; GB:AE001242; GB:AE000520; NID:g3322976; PIDN:
A;Experimental source: strain Nichols
C;Comment: This protein is a component of an ATP-binding cassette operon involved in gal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gag protein - maize
C;Species: Zea mays (maize)
C;Date: 29-Nov-1995 #sequence_revision 01-Mar-1996 #text_change 29-Oct-1999
C;Accession: S58488
Mol. Gen. Genet. 248, 471-480, 1995
A;Title: Zeon-1, a member of a new maize retrotransposon family.
A;Reference number: S58484; MUID:96004768; PMID:7565611
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                                                                                                                                                                                                                                                                                                                                   ch 51.2%; Score 43.5; DB 2; Length 403; 1 Similarity 55.6%; Pred. No. 8.1; 10; Conservative 1; Mismatches 4; Indels
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114 HNDSKVRTEGIRRALGTW 131
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Best Local Similarity 46.7<sup>1</sup>
Matches 7; Conservative
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Matches 8; Conservative
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61 SPLSTELQATPW 72
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Best Local Similarity
Matches 10; Conserv
A; Residues: 1-403 <COL>
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S58484
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| NNVPIRSERQAT 434
                                                        Query Match
Best Local Similarity 60.0
Matches 6; Conservative
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Best Local Similarity 63.6
Matches 7; Conservative
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Best Local Similarity
Matches 7; Conserv
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    C;Genetics:
A;Gene: RC1210
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                                                                                       A;Cross-references: UNIPROT:P33702; UNIPARC:UP1000012A384; EMBL:Z22646; NID:g605659; PID
C;Superfamily: Rhizobium succinoglycan biosynthesis glycosyltransferase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Rhizobium meliloti
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: 840175
C;Accession: 840175
R;Becker, A.; Kleickmann, A.; Kuester, H.; Keller, M.; Arnold, W.; Puehler, A.
submitted to the EMBL Data Library, April 1993
A;Description: Analysis of the Rhizobium meliloti genes exoU, exoV, exoW, and exol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 9
B97851
hypothetical protein RC1210 [imported] - Rickettsia conoxii (strain Malish 7)
C;Species: Rickettsia conoxii
C;Species: Rickettsia conoxii
C;Species: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C;Accession: B97851
R;Ogata, H., Audic., S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, Science 293, 2093-2098, 2001
A;Title: Mechanisms of Evolution in Rickettsia conoxii and Rickettsia prowazekii.
A;Reference number: A97700; MUID:21442074; PMID:11557893
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 319
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A; Reference number: A95842; MUID:21396508; PMID:11481431
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Pred. No. 12;
1; Mismatches
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S40175
ExoW protein - Rhizobium meliloti
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Matches 8; Conservative
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hes 8; Conserv
                A, Accession: A95976
A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-319 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A, Accession: S40175
A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-319 < BEC>
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A;Molecule type: DNA
A;Residues: 1-101 <KUR>
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A;Gene: exoW; SMb21690
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C;Accession: B85066
R;anonymous, The Buropean Union Arabidopsis Genome Sequencing Consortium, The Cold Sprin. Nature 402, 769-777, 1999
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidópsis thaliana. A;Reference number: A85001; MUID:20083488; PMID:10617198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Status: preliminary
A,Modecule type: DNA
A,Modecules: 1-259 (STD>
A,Fodecules: 1-259 (STD>
A,Cross_references: UNIPROT:Q9M0W9; UNIPARC:UPI00000A640D; GB:NC_001268; NID:g7267286; P
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A;Cross-references: UNIPROT:Q9U3L2; UNIPARC:UPI00001641A7; EMBL:Z68215; PIDN:CAB54213.1;
A;Experimental source: clone C53B4
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A,Introns: 15/3; 92/2; 252/3; 306/1; 477/2; 571/1; 605/1; 720/3; 880/3; 1008/2; 1091/1;
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                                                                                                                                                                                                                                                                             hypothetical protein AT4g05260 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein C53B4.4c - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Dec-2004
                          Gaps
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C;Species: Caenorhabditis elegans
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A,Molecule type: DNA
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58.3%; Pred. No. 92;
tive 4; Mismatches
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A;Reference number: 219233
ed. No. 4.9;
Mismatches
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A;Residues: 1-151 <PAR>
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R;Parthill, J: Dougan, G:;James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov A;Accession: AF0931
A;Accession: AF0931
A;Status: preliminary
A;Molecule type: DNA
                                                                                                             A;Reference number: 219233
A;Accession: T20180
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1584 *MIL>
A;Cross-references: UNIPROT:Q18798; UNIPARC:UP100002A219; EMBL:Z68215; PIDN:CAA92457.1;
A;Experimental source: clone C53B4
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A;Residues: 1-1586 <WIL>
A;Cross-references: UNIPROT:Q18798; UNIPARC:UPI0000866B7; EMBL:Z68215; PIDN:CAA92456.1;
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A,Introns: 61/2; 150/3; 227/2; 387/3; 441/1; 612/2; 706/1; 740/1; 855/3; 1015/3; 1143/2;
C;Superfamily: Caenorhabditis elegans hypothetical protein C53B4.4c
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A;Introns: 61/2; 150/3; 227/2; 387/3; 441/1; 612/2; 706/1; 740/1; 855/3; 1015/3; 1145/2;
C;Superfamily: Caenorhabditis elegans hypothetical protein C53B4.4c
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T20179
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004 C;Accession: T20180 C;Accession: T20180 RS;Berks, M. submitted to the EMBL Data Library, December 1995
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58.3%; Pred. No. 1e+02;
iive 4; Mismatches 1; Indels
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A;Reference number: Z19233
A;Accession: T20179
A;Status: preliminary; translated from GB/EMBL/DDBJ
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558 NNVPIRSERQAT 569
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glucosamine-6-phosphate deaminase (EC 3.5.99.6) - Haemophilus influenzae (strain Rd KW20 C;Species: Haemophilus influenzae C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004 C;Accession: F64050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Cross_references: UNIPROT:P44538; UNIPARC:UPI000012FD06; GB:U32700; GB:L42023; NID:g32
C;Superfamily: glucosamine-6-phosphate isomerase
C;Keywords: hydrolase; isomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RiFleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, B.F.; Kerlavage, P. Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.D.; Baradon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Reference number: A64000; MUID:95350630; PMID:7542800
A;Cross-references: UNIPARC:UPI000013C475; GB:AL513382; PIDN:CAD09472.1; PID:g16504589; C;Genetics:
A;Gene: STY3713
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Pred. No. 12;
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Best Local Similarity
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05e2f3
04pfk4
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Q4znl8
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Q67j75
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              GenCore version 5.1.9 (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                           2849598 seqs, 925015592 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65 CQB3 CRYPV

08XXG1 FALSO

07PCB5 GOSAR

094189 CRYNE

094189 CRYNE

0955R83 CRYNE

055R87 CRYNE

055R87 CRYNE

05087 DROME

08MTZ6 DROME

08MTZ6 DROME

0608Z5 DROME

0608Z5 DROME

0608Z5 DROME

063KF24 BEEPF

1603KF24 B
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Q2SBJB 9GAMM
SYE_CAUCR
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Q8JIW9 XENLA
Q5E2F3 VIBF1
Q4PFK4 USTMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q4ZNL8 PSEU2
Q87WK0 PSESM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q4WH60 ASPFU
Q9VW10 DROME
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Q4SZV7_TETNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q87WK0_PSESM
Q67J75_SYMTH
                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                              OM protein - protein search, using sw model
                                                                                                                                                                                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*
                                                                                                                                                                                                                    1 HNDSPVRTEQQATTW 15
                                                                                                                                                                                                                                                                                                                                                                              length: 0
length: 2000000000
                                                                                                                                                                                   US-10-758-165A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query
Match Length DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Minimum DB seq
Maximum DB seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Perfect score:
                                                                                                                                                                                                                                                          Scoring table:
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                                                                                                                                                                                                                         Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Database
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ö
            446215 trypanosoma

884948 anabaena sp

07326 mycobacteri

073260 zea mays (m

896120 homo sapien

P33702 thizobium m

06666 yarrowia 11

07410 anopheles g

06bgk5 paramecium

061046 photobacter

062p11 mus musculu

049776 ustilago ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;
Tetrahymenina; Tetrahymenidae; Tetrahymena.
NCBI_TaxID=5911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AYS60586; AAS55115.1; Genomic_DNA.

R HSSP; P24941; IKE8

GO; GO:0000166; F:NUCleotide binding; IEA.

GO; GO:0001674; F:Protein serine/threonine kinase activity; IEA.

GO; GO:0016740; F:transferase activity; IEA.

GO; GO:0006748; F:Nucleoniae.

R InterPro; IPR001245; Tyr_pkinase.

R InterPro; IPR001245; Tyr_pkinase.

R Prodom; P0000001; Prot Linase; 1.

R PROSITE; PS00107; PROTEIN KINASE_DOW; 1.

R PROSITE; PS00107; PROTEIN KINASE_DOW; 1.

R PROSITE; PS00107; PROTEIN KINASE_DOW; 1.

R PROSITE; PS00108; RATEIN KINASE_DOW; 1.

R PROSITE; PS00108; RATEIN KINASE_ST; 1.

M ATP-binding; Kinase; Nucleotide-Dinding;

M Serine/threonine-protein kinase; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arslanyolu M., Yildiz M.T.;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58.8%; Score 50; DB 2;
64.3%; Pred. No. 5.9;
live 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-JUL-2004, integrated into UniProtKB/TrEMBL 05-JUL-2004, sequence version 1. PFBB-2006, entry version 16. Mitogen activated protein kinase 4.
                                                                                                                                                                                                                                                                                                                                                                                                                      397 AA
                                                    Q73SZE_MYCPA
Q7XBDQ_MAIZE
ZN75A_HUMAN
EXOW_RHIME
Q6CGGE_ARLI
Q7Q1AQ_ANOGA
Q6EGKS_PARTE
                                                                                                                                                                                            OGLNOG PHOPR
OGZPN1 MOUSE
O4P7R6 USTMA
                                                                                                                                                                                                                                                                                                                   ALIGNMENTS
                    TRYCR
                                                                                                                                                                                                                                                           Q96VE8 USTMA
                Q4E215
Q8YWK9
                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :|:||||| || DDNPVRTEYVATRW 182
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2221
2222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           retrahymena thermophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
les 9; Conserv
QGQ4A6_TETTH
QGQ4A6;
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us-10-758-165a-2.rup

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EMBL, AL646068; CAD15860.1; -; Genomic_DNA.

BioCyc; RSOL305:RSC2153-MONOMER; -
GO, GO:0016597; F:amino acid binding; IEA.
GO; GO:0016597; F:amino acid binding; IEA.
GO; GO:0016597; F:amino acid binding; IEA.
GO; GO:0016787; F:quanosine-3',5'-bis(diphosphate) 3'-diphosp. .; IEA.
GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:0016787; F:transferase activity; IEA.
GO; GO:0016787; F:transferase activity; IEA.
GO; GO:001596; P:amstaport; IEA.
GO; GO:001596; P:metabolism: IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons, rosids, eurosids II; Malvales, Malvaceae, Malvoideae, Gossypium.
Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Siquier P., Thebault P., Whalen M., Wincker P., Levy M., Weissenbach J., Boucher C.A.; Genome sequence of the plant pathogen Ralstonia solanacearum."; Nature 415:497-502(2002).

-! FUNCTION: In eubacteria ppGpp (guanosine 3'-diphosphate 5-'diphosphate) is a mediator of the stringent response that coordinates a variety of callular activities in response to changes in nutritional abundance. This enzyme catalyzes the formation of pppGpp which is then hydrolyzed to form ppGpp (By
                                                                                                                                                                                                                                                                                                                                                                   CATALYTIC ACTIVITY: ATP + GTP = AMP + guanosine 3'-diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lorbiecke R., Sauter M.M.; "Comparative analysis of PSK peptide growth factor precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIGRFAMS; TIGR00691; spoT_relA; 1.
Complete proteome; Hydrolase; Kinase; Transferase.
SEQUENCE 735 AA; 81862 MW; 9A6B0054104FD241 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56.5%; Score 48; DB 2; 53.3%; Pred. No. 26; ive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-DEC-2003, integrated into UniProtKB/TrEMBL.
15-DEC-2003, sequence version 1.
07-FEB-2006, entry version 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- PATHWAY: ppGpp metabolism; first step.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Putative phytosulfokine peptide precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002912; ACT_bd.
InterPro; IPR012675; Perredoxin_fold.
InterPro; IPR006674; HD_hydro.
InterPro; IPR003607; Met_phos hydro.
InterPro; IPR007685; RelA_SpoT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR004811; SpoT_relA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGS-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF01842; ACT; 1.
Pfam; PF01966; HD; 1.
Pfam; PF04607; RelA_SpoT; 1.
Pfam; PF02824; TGS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    358 ННОВРОКАОООАНОМ 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 HNDSPVRTEQOATTW 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR004095; TGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00471; HDc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; IPR012676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=29729;
                                                                                                                                                                                                                                                                                                                                                                                                 triphosphate.
                                                                                                                                                                                                                                                                                                                                        similarity)
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Q7PCB5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=PSK1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro
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                                                                                                                                          12-APR-2005, sequence version 1.
21-FEB-2006, entry version 9.
Possible ABC transporter with AAA domain and 12 transmembrane domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ٦.
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ATP-binding; Membrane; Nucleotide-binding; Transmembrane; Transport.
SEQUENCE 1522 AA; 176017 MW; 75C04515093B3981 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : (P) PPGPP SYNTHETASE II AND GUANOSINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=Iowa type II;
bubdel=1044751, DOL=10.1126/Science.1094786;
Abrahamsen M.S., Templeton T.J., Enomoto S., Abrahante J.E., Zhu G.
Lancto C.A., Deng M., Liu C., Widmer G., Tzipori S., Buck G.A., Xu
Bankier A.T., Dear P.H., Konfortov B.A., Spriggs H.F., Iyer L.,
Anantharaman V., Aravind L., Kapur V.,
"Complete genome sequence of the apicomplexan, Cryptosporidium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21681879; PubMed=11823852; DOI=10.1038/415497a; Aslanoubbar M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L., Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.,5-BISDIPHOSPHARE 3.-PYROPHOSPHOHYDROLASE (PPGPPASE) PROTEIN (EC 2.7.6.5) (EC 3.1.7.2).
Name=spor; OrderedLocusNames=RSc2153; ORFNames=RS01611; Namespor; OrderedLocusNames=RSc2153; ORFNames=RS01611; Bacteria solanacearum (Peaudomonas solanacearum).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     parvum.";
Science 304:441-445(2004).
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ô
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Indels
                                                                                                                                                                                                                                      ORFNames=cgd4_1190;
Cryptosporidium parvum.
Bukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
Cryptosporidiidae; Cryptosporidium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AAEB01000009; EAKB7614.1; -; Genomic_DNA. GO; GO:0016021; C:integral to membrane; IEA. GO; GO:0005524; F:ATP binding; IEA. GO; GO:0016887; F:ATPase activity; IEA. GO; GO:000166; F:nucleotide binding; IEA. InterPro; IRR00359; AAA_ATPase.
InterPro; IRR003499; ABC_transp_like.
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                                                                                                        12-APR-2005, integrated into UniProtKB/TrEMBL
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                                               PRT; 1522 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58.8%; Score 50; DB 53.3%; Pred. No. 26; ive 2; Mismatches
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NCBI_TaxID=305;
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Q8XXG1;
                                            PRELIMINARY;
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HNDKQVRPESEISTW 86
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Best Local Similarity 53...
8; Conservative
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                                            QSCQB3_CRYPV
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Length 735; Indels

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O94188 CRYNE
O94188;
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Q55R83;
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GO; GO:0016301; F:kinase activity; IEA.
GO; GO:0016773; F:phosphotransferase activity, alcohol group . . .; IEA.
GO; GO:0016740; F:transferase activity; IEA.
                                                                                                         Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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MEDLINE=99562981; PubMed=10330150;
Cruz M.C., Cavallo L.M., Gorlach J.M., Cox G., Perfect J.R.,
Cardenas M.E., Heitman J.;
"Rapamycin antifungal action is mediated via conserved complexes with
FKBP12 and TOR kinase homologs in Cryptococcus neoformans.";
Mol. Cell. Biol. 19:4101-4112(1999).
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Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
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homologs.";
Plant Sci. 163:321-332(2002).
-!- MISCELLANEOUS: The sequence shown here is derived from an EMBL/GenBank/DDBJ third party annotation (TPA) entry.
                                                                                                                                                                                                                                                                                                                                                                                        Score 47; DB 2; Length 84; Pred. No. 3.6; 3; Indels 2; Mismatches
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                                                                                                                                                                                                                                                                                                                           Potential.
6B04F8D05EC36C9B CRC64;
                                                                                                                                                                    EMBL; BK000114; DAA00278.1; -; mRNA.
GO; GO:0005576; C:extracellular region; IEA.
GO; GO:0008083; F:growth factor activity; IEA.
GO; GO:0008283; P:cell proliferation; IEA.
InterPro; IPR009438; PSK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-1999, integrated into UniProtKB/TrEMBL.
01-MAY-1999, sequence version 1.
07-ERB-2006, entry version 29.
Phosphatidylinositol 3-kinase TORI (Fragment).
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InterPro; IPR003151; FAT.
InterPro; IPR000403; P13/4 kinase cat.
InterPro; IPR011990; TPR-like_helical.
Pfam; PF02250; FAT; 1.
Pfam; PF02260; FATC; 1.
Pfam; PF0454; P13 P14 kinase; 1.
PR05ITE; PS00915; P13 A KINASE 1; 1.
PR05ITE; PS00915; P13 A KINASE 1; 1.
Kinase; Transferase.
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HSSP; P42345; 1AUE.
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84 AA; 9242 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                61.5%;
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NDSPAKTQSQGTT 44
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                                                                                                                                                                                                                                                                                                                                                                                                                                  8; Conservative
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094189;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=99262981; PubMed=10330150; Cruz M.C., Cavallo L.M., Gorlach J.M., Cox G., Perfect J.R., Cardenas M.C., Heitman J.; Rapamycin antifungal action is mediated via conserved complexes with FKBP12 and TOR kinase homologs in Cryptococcus neoformans."; Mol. Cell. Biol. 19:4101-4112(1999).
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Tremellomycetidae, Tremellales, Tremellaceae, Filobasidiella.
                                                           Gaps
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GG; GG:0016301; F:kinase activity; IEA.
GG: GG:00173; F:phosphorransferase activity, alcohol group
InterPro; IPR011989; ARM-like.
InterPro; IPR001151; FAT.
     Length 1083;
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                                                        7; Indels
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     2,
                                                                                                                                                                                                                                                                                                                                                     01-MAY-1999, integrated into UniProtKB/TrEMBL. 01-MAY-1999, sequence version 1.
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                                                                                                                                                                                                                                                                                                     PRT; 2360 AA.
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55.3%; Score 47; DB 53.3%; Pred. No. 60; iive 0; Mismatches
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HSSP; P42345; 1AUE.
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Interpro; IPR00152; FATC.
Interpro; IPR000157; HEAT.
Interpro; IPR011990; PI3/4 kinase_cat.
Interpro; IPR011990; PR-like_helical.
Pfam; PF02259; FATC; 1.
Pfam; PF02259; FATC; 1.
Pfam; PF00454; PI3 PI4 kinase; 1.
SMART; SM00146; PI3 RC; 1.
PROSITE; PS00915; PI3 4 KINASE 1; 1.
PROSITE; PS00915; PI3 4 KINASE 1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Phosphatidylinositol 3-kinase TOR1.
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                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                               202 HADEPARQEMOROTW 216
                                                                                                         1 HNDSPVRTEQQATTW 15
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  Query Match
Best Local Similarity 53.3
Matches 8; Conservative
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nes 8; Conserv
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The genome of the basidiomycetous yeast and human pathogen
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GO; GO:0005488; F:binding; IEA.
GO; GO:0016773; F:phosphotransferase activity, alcohol group . . .; IEA.
InterPro; IPR011989; ARM-like.
InterPro; IPR00403; P13/4 kinase cat.
InterPro; IPR0011990; TPR-like_helical.
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Distributed under the Creative Commons Attribution-NoDerivs License
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Bukaryota, Fungi, Basidiomycota, Hymenomycetes, Heterobasidiomycetes,

Tremellomycetidee, Tremellales, Tremellaceae, Filobasidiella.

NCBI_TaxID=5207;
                                                                 Cryptococcus neoformans var. neoformans B-3501A.
Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
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PubMed=15653466; DOI=10.1126/science.1103773;
PubMed=15653466; DOI=10.1126/science.1103773;
PubMed=15653466; DOI=10.1126/science.110373;
Vamathevan J., Miranda M., Anderson I.J., Fraser J.A., Allen J.B., Boodet I.E., Brent M.R., Chiu R., Doering T.L., Donlin M.J., Huang J.C., Fax D.S., Grinberg V., Fu J., Fukushima M., Haas B.J., Kwon-Chung K.J., Lengeler K.B., Mairli R., Marra M.A., Marra R.E., Mathwoon C.A., Mitchell T.G., Pertea M., Riggs F.R., Salzberg S.L., Schein J.E., Shvartsbeyn A., Shin H., Shumway M., Specht C.A., Shy B.B., Tenney A., Utterback T.R., Mickes B.L., Wortman J.R., Waye N. H., Kronstad J.W., Lodge J.K., Heitman J., Davis R.W.,
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                                                                                                                                                                                                                                                                                                  Fung E., Hyman R.W., Rowley D., Bruno D., Miranda M., Fukushima I
Wickes B.L., Fu J., Davis R.W.;
"Cryptococcus neoformans serotype D sequencing.";
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF02259; FAT; 1.
Pfam; PF02260; FATC; 1.
Pfam; PF02985; HEAT; 3.
Pfam; PF00454; PI3 PI4 kinase; 1.
SMART; SM00146; PI3KC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1479 HADEPAROEMOROTW 1493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Query Match
Best Local Similarity 53.30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           preliminary data.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein.
          Hypothetical protein.
ORFNames=CNBF1080;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2360 AA;
                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
                                                                                                                                                                      NCBI_TaxID=283643;
                                                                                                                                                                                                                                                                             STRAIN=B-3501A;
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QSKEY7;
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SEQUENCE 23
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NEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185; Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amaratides P.G., Scherer S.E., Lip P.W., Hoskins R.A., Galla R.F., Amaratides P.G., Scherer S.E., Lip P.W., Hoskins R.A., Galla R.F., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Barachar E.G., Rogers Y.-H.C., Blazelj R.G., Change M., Pfeiffer B.D., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Baun A., Baxendale J., Basanley E.M., Ballew R.M., Barand B.P., Bhandari D., Bolshakov S., Ballew R.M., Cawley S., Butler H., Cadieu E., Center A., Chandra I., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Abrits K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Achery J.M., Cawley S., Dalke C., Davenport L.B., Davies P., Achery J.M., Cawley S., Dalke C., Davenport L.B., Davies P., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Goldek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Houston K.A., Heiman T.J., Hernandez J.R., Houck J., Howland T.J., Meatin D., Houston K.A., Heiman T.J., Meatin D., Houston K.A., Howland T.J., Weinlison J.A., Ketchum K.A.,
                                                                                                                      EMBL; AED17346; AAW44029-11; -; Genomic_DNA.

GO; GO:0005488; F: binding; IEA.

GO; GO:0016301; F: Rinase activity; IEA.

GO; GO:0016773; F: phosphotransferase activity, alcohol group . . .; IEA.

InterPro; IPR011989; ARM-like.

InterPro; IPR03151; FAI.
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CG31299-Pb, isoform B.
Name-nocturnin; ORFNames-Dmel_CG31299;
Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hoxapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 2360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55.3%; Score 47; DB 2; Length 236
53.3%; Pred. No. 1.4e+02;
iive 0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             267304 MW; EB7ABF966AB68ADF CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR003152; FATC.
InterPro; IPR003152; FATC.
InterPro; IPR000403; P13/4 kinase_cat.
InterPro; IPR011990; TPR-11ke_helical.
Pfam; PF02259; FAT; 1.
Pfam; PF02286; FATC; 1.
Pfam; PF02985; HEAT; 3.
Pfam; PF00454; P13 P14 kinase; 1.
SMART; SM00146; P13 P14 kinase; 1.
PROSITE; PS00915; P13 4 KINASE_1; 1.
PROSITE; PS50290; P13 4 KINASE_1; 1.
Complete; PS50290; P13 4 KINASE_3; 1.
Complete; PS50290; P13 4 KINASE_3; 1.
SMGUENCE 2360 AA; 267304 MW; EB7ABF96
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Cryptococcus neoformans."; Science 307:1321-1324(2005).
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nes 8; Conservative
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Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Liasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X., Liu X., Martei B. W., McIrod M.P., McDrenson D., Merkulov G., Milahina N.V., Mobarry C., Morris J., Moshrefi A., Merkulov G., Milahina N.V., Mobarry C., Morris J., Moshrefi A., Mason D.K., Nelson D.K., Nakson K., Naskern D.R., Pacled J.M., Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Rese M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Spier B., Spradling A.C., Turner R., Vencer E., Wang A.H., Wang X., Wang Z.-Y. Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Williams S.M., Woodage T., Morley K.C., Wu D., Yang S., Yao Q.A., Abeng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

"The genome sequence of Drosophila melanogaster.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=22426065; PubMed=12537568;
Celniker S.B., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise B., Hodgon A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C., Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.; Finishing a whole-genome shotgun: release 3 of the Drosophila melanogaster euchromatic genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-22446069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.G., Milburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.
Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE.

Berkeley Drosophila Genome Project;
Celniker S., Carlson J., Wan R., Pfeiffer B., Frise E., George R.,
Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.
Yu C., Rubin G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Drosophila melanogaster release 4 sequence.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE003690; AAF54601.2; -; Genomic_DNA.
Flybase; FBgn0037872; nocturnin.
InterPro; IPR005135; Exo-endo_phos.
Pfam; PF0372; Exo-endo_phos; 1.
SEQUENCE 425 AA; 47584 MW; AABF2F745411D29F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      systematic review.";
Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Identification of four families of yCCR4- and Mg2+-dependent endonuclease-related proteins in higher eukaryotes, and characterization of orthologs of yCCR4 with a conserved leucine-rich repeat essential for hCAF1/hPoP2 binding.";

BMC Genomics 2:9-9(2001)
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                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                   Pacleb J.,
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Eukaryota, Metazoa, Arthropoda; Haxapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda, Hexapoda; Insecta; Pterygota;
Neoptera; Endopteryyota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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MEDLINE=22730715; PubMed=11747467;
Dupressoir A., Morel A.-P., Barbot W., Loireau M.-P., Corbo
Heidmann T.;
                                                                                                                                                                                                                                                                                                                                                                                Stapleton M., Carlson J., Chavez C., Frise E., George R., Park S., Wan K., Yu C., Celniker S.; Submitted (AUG-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 446;
             Length 425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Indels
                                         Indels
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                                                                                                                                                                                             27-SEP-2005, integrated into UniProtKB/TrEMBL. 27-SEP-2005, sequence version 1. 07-FEB-2006, entry version 3.
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                                                                                                                                                                    446 AA.
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                                       2; Mismatches
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             Score 46;
Pred. No.
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InterPro; IPR005135; Exo endo phos.
Pfam, PF03372; Exo endo phos; 1
SEQUENCE 446 AA; 49953 WW; 1F694)
                                                                                                                                                                  PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=nocturnin; ORFNames=CG31299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence version 1.
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             54.1%;
                                                                                                                                                                    PRELIMINARY;
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109 HNDGFVRCPEEALTW 123
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                                                                    1 HNDSPVRTEQOATTW 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 HNDSPVRTEQOATTW 15
8; Conservative
                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Berkeley;
                                                                                                                                                                                                                                                       Name=nocturin;
                                                                                                                                                                  Q3ZAP4 DROME
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QBMTZ6;
                                                                                                                                                                                                                                         RE65127p.
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Genome Biol. 3: RESEARCH0083.1-RESEARCH0083.22(2002).
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Attribution-NoDerivs License
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07-FEB-2006, entry version 19.
CG31299-PA, isoform A.
Name=nocturnin; ORFWames=Dmel CG31299;
Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Bohydroidea; Drosophilidae; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=nocturnin, Synonyms=nocturin,
Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera; Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
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                                                                                                                                                                                                                                                                   54.1%; Score 46; DB 2; Length 449;
53.3%; Pred. No. 35;
iive 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Indels
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FlyBase; FBgn0037872; nocturnin.
InterPro; IPR005135; Exo-endo_phos.
Pfam; PF0372; Exo-endo_phos; 1.
SEQUENCE 526 AA; 58951 MW; BDE221244AB110FA CRC64;
                                                                                                                FlyBase; PBgn0037872; nocturnin.
InterPro; IRR005135; Exo endo phos.
Pfam; PF03372; Exo endo phos; 1.
SEQUENCE 449 AA; 50275 WW; 1607DF25A418A024 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-SEP-2004, integrated into UniProtKB/TrEMBL.
13-SEP-2004, sequence version 1.
07-FEB-2006, entry version 9.
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Copyrighted by the UniProt Consortium, Distributed under the Creative Commons
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Q9VGSS;
                                                                                    EMBL; AY043266; AAK85704.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                               133 HNDGFVRCPEEALTW 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 HNDSPVRTEQQATTW 15
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                                                                                                                                                                                                                                                                                                  Local Similarity 53.3
nes 8; Conservative
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06AWF6 DRO
106AWF
AC 06AWF
AC 06AWF
DT 13-SF
DT 13-SF
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0904GS5 DRC
10 0904GS
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AC 0904GS
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DT 01-AP
DT 07-FF
DE CG31,
GN Name-
OC Name-
OC Rebay
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OC REPAY
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MEDLINE-Z0196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185; RA Amanatides P. Calnikers S.E. Holt R.A., Evans C.A., Gocayne J.D., RA Amanatides P. Calnikers S.E., Holt R.A., Evans C.A., Gocayne J.D., Rad C., Rotten G.C., Northand J.R., P.W., Hoskins R.A., Galle R.F., Garles R.A., Levis S.E., Is live, Holf G., Change M., Pfeifer B.D., RA Brandon R.C., Northand J.R., Palazel R.G., Change M., Pfeifer B.D., RA Brandon R.C., Rogers Y.-H.C., Blazel R.G., Nolson C.R., Miklos G.L.G., Abril J.F., Agbayani A., And Teves Pfennkoch C., Baladin D., RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Besaley E.M., Ballew R.M., Bacos A., Baxendale J., Bayraktaroglu L., Besaley E.M., RA Beson K.I., Benos P.V., Berman B.P., Brottier P., Randing N.J., Wellen P., Heir M., Hausten P., Rarvitz S., Kulp D., Lai Z., Liang Y., Lasko P., Lei Y., Levitsky A.A., Li J.H., Marrits M., Nelson D.L., Martei B., McIntosh T.C., McIecod M.P., Morthy L., Murphy L., Murphy L., Murphy L., Martei B., McIntosh T.C., McLeod M.P., Palazolo M., Pittman G.S., Pan S., Pollaku V., Walsen B.C., Shander R., Wang Z.-Y., Wassarman D.A., Weinster B., Wang Z.-Y., Wassarman D.A., Weinster B., Wang Z.-Y., Wassarman D.A., Weinster E., Wang G., Yan, Woolfey K.C., Wan W. D., Weinster P., Walley C., Sanith H., Sheng K.H., Brong
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NUCLEOTIDE SEQUENCE.
NUCLEOTIDE SEQUENCE.
NUCLEOTIDE SEQUENCE.
NUCLEOTIDE S. 22426070; PubMed=12537573;
Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R., Ratinker J.S., Brise E., Wheeler D.A., Lewis S.E., Rubin G.M., Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E.;
Ashburner M., Celniker S.E.;
"The transposable elements of the Drosophila melanogaster euchromatin:
"The transposable elements of the Drosophila melanogaster euchromatin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Venter C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
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Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
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Query Match
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Q48E23_PSE14
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GO; GO:0016020; C:membrane; IEA.

GO; GO:0016469; C:proton-transporting two-sector ATPase complex; IEA.

GO; GO:0046931; F:hydrogen-transporting ATP synthase activity. . .; IEA.

GO; GO:0015986; P:hydrogen-transporting ATPase activity, rota. . .; IEA.

GO; GO:0015986; P:ATP synthesis coupled proton transport; IEA.

GO; GO:0015922; P:proton transport; IEA.
                                                                                                                                                                                                                                                                                                                                    Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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                                           Berkeley Drosophila Genome Project;
Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
Celniker S., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.
Yu C., Rubin G.;
"Drosophila melanogaster release 4 sequence.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=GB-M1;
MEDLINE=215:6510; PubMed=11719806; DOI=10.1038/35106579;
Ratinka M.D., Duprat S., Cornillot E., Metenier G., Thomarat F., Prensier G., Barbe V., Peyretaillade E., Brottier P., Wincker P., Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M., Weissenbach J., Vivares C.P.;
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VACUOLAR AIP SYNTHASE 95kDa SUBUNIT.
OrderedLocusNames=ECUO9 1790;
Encephalitozoon cuniculi.
Encephalitozoon y Microsporidia; Unikaryonidae; Encephalitozoon.
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Pred. No. 49;
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                                                                                                                                                                                                                                                        FlyBase;
Submitted (JAN-2006) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE003690; AAF54600.2; -; Genomic_DNA.
FlyBase; FBGn0037872; nocturnin.
InterPro; IPR005135; Exo_endo_phos.
Pfam; PF03772; Exo_endo_phos; 1.
SEQUENCE 621 AA; 69511 MW; A775AD0BB776FEF1 CRC64;
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PROSITE; PS00079; MULTICOPPER_OXIDASE1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2002, integrated into UniProtKB/TrEMBL.
01-JUN-2002, sequence version 1.
07-FEB-2006, entry version 18.
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GO; GO:0016469; C:proton-transporting two-
GO; GO:0046933; F:hydrogen-transporting AT
GO; GO:0046961; F:hydrogen-transporting AT
GO; GO:0015986; P:ATP synthesis coupled px
GO; GO:0015992; P:proton transport; IEA.
InterPro; IPR00215; Cu oxidase Cu BS.
InterPro; IPR00235; Cu oxidase Cu BS.
InterPro; IPR002490; V ATPase_sub116.
PANTHER; PTHR11629; V ATPase_sub116.
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nes 8; Conservative
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                        NUCLEOTIDE SEQUENCE.
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SEQUENCE 700 AA
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OSSONG ENC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

PubMed=16159782; DOI=10.1128/JB.187.18.6488-6498.2005;

PubMed=16159782; DOI=10.1128/JB.187.18.6488-6498.2005;

PubMed=16159782; DOI=10.1128/JB.187.18.6488-6498.2005;

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Mansfield J., Collmer A., Buell R.;

Mansfield J., Collmer A., Buell R.;

phassolicola 1448A reveals divergence among pathovars in genes
involved in virulence and transposition.";

J. Bacteriol. 187:6488-6498(2005).
                                                                    Gaps
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Hypothetical protein.
OrderedLocushanes=PSPPH 4249;
Pseudomonas syringae pv. phaseolicola (strain 1448A / Race 6).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
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Score 45.5; DB 2; Length 700;
Pred. No. 69;
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                                                                    Indels
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Complete proteome; Hypothetical protein.
SEQUENCE 79 AA; 8809 MW; D167EB243339F201 CRC64;
                                                                    4;
                                                                                                                                                                                                                                                                                                                                                                                                           13-SEP-2005, integrated into UniProtKB/TrEMBL 13-SEP-2005, sequence version 1.
                                                                                                                                                                                                                                                                                                                                                    79 AA.
                                                                    2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY; PRT;
                                                                                                                                                                                        233 HNDEAIRKEQEKIRHFANTW 252
                                                                                                                                 1 HNDSPVRTEQO----ATTW 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pseudomonadaceae; Pseudomonas.
      Query Match
Best Local Similarity 45.0%;
Matches 9; Conservative
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nes 8; Conservative
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Sequence 29, Appl
Sequence 37, Appl
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 45.29, A
Sequence 8, Appli
Sequence 8, Appli
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Seguence 2, Appli
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                                                                                                                                                                             August 30, 2006, 04:31:13; Search time 14.8485 Seconds (without alignments) 88.424 Million cell updates/sec
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/EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
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/EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-09-479-614-29
US-09-281-760E-37
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US-08-336-583-2
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US-09-413-231-8
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US-09-270-767-39006
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         650591 seqs, 87530628 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                        OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length DB
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27 38 44.7 127 2 US-09-270-767-54233 Sequence 54223, A PAPLI 29 3 44.7 127 2 US-09-784-340-2 Sequence 5. Appli 30 44.7 527 3 US-09-784-340-5 Sequence 5. Appli 31 34 44.7 527 3 US-10-114-270-5 Sequence 5. Appli 32 38 44.7 528 2 US-09-784-340-5 Sequence 5. Appli 34 44.7 528 2 US-09-356-606 Sequence 5. Appli 34 44.7 528 2 US-09-366-606 Sequence 6. Appli 35 38 44.7 528 2 US-09-366-606 Sequence 6. Appli 36 44.7 528 2 US-09-366-606 Sequence 6. Appli 36 44.7 528 2 US-09-366-606 Sequence 6. Appli 36 44.7 528 2 US-09-366-609 Sequence 6. Appli 36 44.7 528 2 US-09-144-00-5324-5612 Sequence 5. Appli 38 44.7 630 2 US-09-144-00-5324-5619 Sequence 6. Appli 37 43.5 44.1 1124 2 US-09-144-00-60-691 Sequence 6. Appli 39 7.5 44.1 1124 2 US-09-144-00-60-691 Sequence 6. Appli 39 7.5 44.1 1124 2 US-09-144-00-60-691 Sequence 6. Appli 39 7.5 44.1 1124 2 US-09-560-901-296 Sequence 6. Appli 39 7.5 44.1 1124 2 US-09-560-901-296 Sequence 6. Appli 37 43.5 113 2 US-09-560-901-296 Sequence 6. Appli 42 37 43.5 113 2 US-09-511-996 Sequence 6. Appli 43 7 43.5 113 2 US-09-111-296 Sequence 6. Appli 44 37 43.5 24.9 2 US-09-11-296 Sequence 6. Appli 44 37 43.5 24.9 2 US-09-11-296 Sequence 6. Appli 44 37 43.5 24.9 2 US-09-11-296 Sequence 6. Appli 44 37 43.5 24.9 2 US-09-11-296 Sequence 6. Appli 44 37 43.5 24.9 2 US-09-11-296 Sequence 6. Appli 44 37 43.5 24.9 2 US-09-11-296 Sequence 6. Appli 44 37 43.5 24.9 2 US-09-11-296 Sequence 6. Appli 44 37 43.5 24.9 2 US-09-11-20-296 Sequence 6. Appli 44 37 43.5 24.9 2 US-09-11-20-296 Sequence 6. Appli 44 37 43.5 24.9 2 US-09-11-20-296 Sequence 6. Appli 44 31.7 EARLINE APPLICATION NUMBER: 60/115.033 SEQUENCE: PLOY NUMBER: 60/115.033 SEQUENCE: PLO	27 38 44.7 28 38 44.7 39 38 44.7 39 38 44.7 31 38 44.7 31 38 44.7 32 38 44.7 33 38 44.7 34 38 44.7 35 38 44.7 36 38 44.7 37 43.5 40 37.5 44.1 40 37.5 44.1 41 37 43.5 42 37 43.5 42 37 43.5 42 37 43.5 42 37 43.5 42 37 43.5 42 37 43.5 42 37 43.5 42 37 43.5 42 37 43.5 43 5 37 5 44.1 44 37 43.5 42 37 43.5 43 5 37 43.5 44 37 43.5 45 37 43.5 45 37 43.5 45 37 43.5 45 37 43.5 45 37 43.5 45 37 43.5 45 37 43.5 45 37 43.5 45 37 43.5 45 37 43.5 45 37 43.5 45 37 43.5 45 37 43.5 45 37 43.5 45 37 43.5 45 37 43.5 45 37 43.5 45 37 43.5 45 37 43.5 45 37 43.5 45 37 43.5 45 37 43.5 45 37 43.5 45 37 43.5 45 37 43.5 45 37 43.5 45 37 43.5 45 37 43.5 45 37 43.5 45 37 43.5 45 37 43.5 45 37 43.5 45 37 43.5 45 37 43.5 45 37 43.5 45 37 43.5 45 37 43.5 45 37 43.5 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.1 47 41.
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Sequence 2, Application US/09479614

Sequence 2, Application US/09479614

Patent No. 6573372

GRNERAL INFORMATION:

APPLICANT: Weber, Eric

TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods

FILE REFERENCE: P-1047

CURRENT APPLICATION NUMBER: US/09/479,614

CURRENT APPLICATION NUMBER: 60/115,033

EARLIER APPLICATION NUMBER: 60/115,033

NUMBER OF SEQ ID NOS: 34

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 2

LENGTH: 496

TYPE: PRT

CREANISM: Felis catus

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PAGES: 282-286
DATE: 1995
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ORGANISM: Dog
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Sequence 29, Application US/09479614

Patent No. 6573737

GENERAL INFORMATION:

APPLICANT: Weber. Eric

ITILE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods

FILE REFERENCE: P-1047

CURRENT FILING DATE: 2000-01-07

EARLIER APPLICATION NUMBER: US/09/479,614

NUMBER OF SEQ ID NOS: 34

SOFTWARE: PATENT OF SEQ ID NOS: 34

SEQ ID NO 29

LENGTH: 496
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APPLICANT: Lawton, Robert
APPLICANT: Lawton, Robert
APPLICANT: Mermer, Brion
APPLICANT: Francour, Gree
TITLE OF INVENTION: Specific Binding Protein for Treating
TITLE OF INVENTION: Canine Allergy
FILE REPERRENCE: 01.1275A
CURRENT APPLICATION NUMBER: US/09/281,760E
CURRENT FILING DATE: 1999-03-30
PRIOR APPLICATION NUMBER: 09/058,331
PRIOR PILING DATE: 1998-04-09
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 37
LENGTH: 108
TYPE: PRT
CORANISM: Canis familiaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 496;
                                  100.0%; Score 85; DB 2; Length 496; 100.0%; Pred. No. 1.2e-06; Live 0; Mismatches 0; Indels
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LOCATION: (136)..(136)
OTHER INFORMATION: "n" stands for any nucleic acid
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc feature
LOCATION: (413)..(414)
OTHER INFORMATION: "n" stands for any nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 85; DB 2; I
100.0%; Pred. No. 1.2e-06;
Live 0; Mismatches 0;
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                                                                           15; Conservative
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Best Local Similarity
Matches 15; Conserve
                                      Query Match
Best Local Similarity
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US-09-479-614-2
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                                                                             Matches
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Sequence 2, Application US/09701623C

Sequence 2, Application US/09701623C

Patent No. 6911782

GENERAL INFORMATION:

APPLICANT: Wang Ph. D., Chang Yi

TITLE OF INVENTION: ALLERGY

TITLE OF INVENTION: ALLERGY

TITLE OF INVENTION: ALLERGY

FILE REFERENCE: 115.14153US1

CURRENT PAPLICATION NUMBER: US/09/701,623C

PRIOR APPLICATION NUMBER: PCT/US99/13959

PRIOR APPLICATION NUMBER: 091100,287

PRIOR FILING DATE: 1998-06-20

PRIOR FILING DATE: 1998-06-20

PRIOR FILING DATE: 1998-06-20

NUMBER OF SEQ ID NOS: 91

SEQ ID NO 2

LENGTH: 312

TANDEL DEPARTED NOS: 91

SEQ ID NO 2

LENGTH: 312
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MAME/KEY: misc_feature
LOCATION: (847)..(849)
OTHER INFORMATION: "n" stands for any nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: misc feature
LOCATION: (853)..(853)
OTHER INFORMATION: "n" stands for any nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc feature
LOCATION: (1382)...(1382)
OTHER INFORMATION: "n" stands for any nucleic acid
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LOCATION: (530)..(530)
OTHER INFORMATION: "n" stands for any nucleic acid
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LOCATION: (568)..(568)
OTHER INFORMATION: "n" stands for any nucleic acid
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                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc feature
LOCATION: (500)..(500)
OTHER INFORMATION: "n" stands for any nucleic acid
OTHER INFORMATION: "n" stands for any nucleic acid
                                                                                                                                                                                                                      stands for any nucleic acid
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Pred. No. 0.65;
3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 61.5%;
Matches 8; Conservative
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44 NDSPIQTDQYTTT 56
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                                                                                                     NAME/KEY: misc feature
LOCATION: (460)..(462)
OTHER INFORMATION: "n"
FEATURE:
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US-09-270-767-45299

Sequence 45299, Application US/09270767

Sequence 45299, Application US/09270767

Sequence 45299, Application US/09270767

GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFRENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT PILING DATE: 1999-03-17

NOWBER OF SEQ ID NOS: 62517

SOUTHARE: PatentIN Ver. 2.0

SEQ ID NO 45299

LENGTH: 210
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Pred. No. 3;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54.1%; Score 46; DB 2; Length 210; 53.3%; Pred. No. 3.1;
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                                     ZIP: 07065-0907

COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
                                                                                                                                                                                                                                              ATTORNEY AGENT INFORMATION:
NAME: CARTY, CHRISTINE E.
REGISTRATION NUMBER: 36,099
REFERENCE/DOCKET NUMBER: 19211Y
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-6734
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 426 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ), ORGANISM: Drosophila melanogaster US-09-270-767-45299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-413-231-8
; Sequence 8, Application US/09413231
; Patent No. 6284483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Dilley, David R
APPLICANT: Kadyrzhanova, Dina K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 149 HNDGFVRCPEEALTW 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56.5%;
ilarity 61.5%;
Conservative
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Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wang, Zhenyong
Warner, Toni M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
  NEW JERSEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCT-US95-13795-2
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
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                                           DB 2; Length 312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application PC/TUS9513795
GENERAL INFORMATION:
APPLICANT: HOLLIS, GREGORY F.
APPLICANT: PATEL, MAYUR D.
TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHRISTINE E. CARTY
STREET: 126 E. LINCOLN AVENUE; P.O. BOX 2000
                                                                                     2; Indels
                                                                                                                                                                                                                                                                                                                             APPLICANT: HOLLS, GREGORY F.
APPLICANT: PATEL, MAYUR D.
TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULIN
NUMBER OF SEQUENCES: 2
CANESPONDENCE ADDRESS:
ADDRESSEE: CHRISTINE E. CARTY
STREET: 126 E. LINCOLN AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIREBLI: 1.2 B. DINCOLN AVENUE
COUTTY: NEW JERSEY
COUNTRY: USA
ZIP: 07055-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURPTATION SYSTEM: US/08/336,583
FLING DATE: 09-NOV-1994
CLASSIFICATION NUMBER: US/08/336,583
FLING DATE: 09-NOV-1994
CLASSIFICATION: 424
ATTORNEY AGENT INFORMATION:
NAME: CARTY, CHRISTINE E.
REGISTRATION NUMBER: 19211
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ ID NO: 2:
SEQUIBLE CHARACTERISTICS:
SEQUIBLE CHARACTERISTICS:
SEQUIBLE CHARACTERISTICS:
SEQUIBLE CHARACTERISTICS:
                                         Score 48; DB 2
Pred. No. 2.1;
3; Mismatches
                                                                                                                                                                                                                                                                    ; Sequence 2, Application US/08336583; Patent No. 5629415; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         126 E. LINCOLN AVENUE
                                         56.5%;
61.5%;
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NDSPIQTDQYTTT 370
                                                                                                                                              ||||::|:|
256 NDSPIQTDQYTTT 268
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Best Local Similarity 61.59
                                                                                                                          2 NDSPVRTEQOATT 14
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                                   Query Match 56.5
Best Local Similarity 61.5
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-336-583-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: RAHWAY
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PCT-US95-13795-2
US-09-701-623C-2
                                                                                                                                                                                                                            RESULT 6
US-08-336-583-2
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Query Match
Best Local Similarity 57.1%;
Matches 8; Conservative
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NAGAI, KEIICHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
US-10-104-047-3886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 6; Conserv
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US-09-24-841-8
US-09-24-841-8

| US-09-24-841-8
| Patent No. 7029888
| Patent No. 7029888
| GENERAL INFORMATION:
| APPLICANT: Dilley, David R
| APPLICANT: Wang, Zhenyong |
| TILE OF INVENTION: Modified Synthetases To Produce Penicillins and |
| TILE OF INVENTION: Modified Synthetases To Produce Penicillins and |
| TILE REPRENCE: MSU41-453 |
| CURRENT FILING DATE: 2001-08-08 |
| PRIOR FILING DATE: 2001-08-08 |
| PRIOR FILING DATE: 1999-10-06 |
| SOFTWARE: PatentIn Ver. 2.0 |
| SOFTWARE: PatentIn Ver. 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Description of Artificial Sequence: modified IPNS OTHER INFORMATION: from Streptomyces cattleya NAME/KEY: MUTAGEN
TITLE OF INVENTION: Modified Synthetases To Produce Penicillins and TITLE OF INVENTION: Cephalosporins Under the Control of Bicarbonate FILE REFERENCE: MSU41.453
CURRENT APPLICATION NUMBER: US/09/413,231
CURRENT FILING DATE: 1999-10-06
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.0
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Pred. No. 7.4;
4; Mismatches 3; Indels
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Pred. No. 7.4;
4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (211)
COTHER INFORMATION: Glu211 in native IPNS modified to Arg
US-09-413-231-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; LOCATION: (211)
; OTHER INFORMATION: Glu211 in native IPNS modified to Arg
US-09-924-841-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 11
US-09-270-767-43758
; Sequence 43758, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52.9%;
50.0%;
                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |:| |:|||
61 NESTTMTDQRSTTW 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 NDSPVRTEQQATTW 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 NESTIMIDORSTIW 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 NDSPVRTEQOATTW 15
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Best Local Similarity 50.07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                  SEQ ID NO 8
LENGTH: 321
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TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT PAPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 43758
LENGTH: 181
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                                                                                                                                                                                                                                                                                                                                      Length 181;
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                                                                                                                                                                                                                                                                                                                                                                                     Indels
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APPLICANT: HELIX RESEARCH INSTITUTE
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: NO. 6943241e1 full length cDNA
FILE REFERENCE: H1-40105
CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT FILING DATE: 2002-03-25
PRIOR PILING DATE:
PRIOR FILING DATE:
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                      Score 44; DB 2;
Pred. No. 5.8;
2; Mismatches
                                                                                                                                                                                                                                                                    , OTHER INFORMATION: Xaa means any amino acid US-09-270-767-43758
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2367, Application US/10094749
Patent No. 6979557
GENERAL INFORMATION:
APPLICANT: ISCGAL, TAKAO
APPLICANT: OTSUKI, TETSUJI
APPLICANT: OTSUKI, TETSUJI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: ISHII, SHIZUKO
APPLICANT: ISHII, SHIZUKO
APPLICANT: YAMAMOTO, UUN-ICHI
APPLICANT: YAMAMOTO, VUUKO
APPLICANT: HISONO, YUUKO
APPLICANT: HISONO, YUUKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3886, Application US/10104047 Patent No. 6943241
                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Drosophila melanogaster
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TAMECHIKA, ICHIRO
SEKI, NAOHIKO
YOSHIKAWA, TSUTOWU
OTSUKA, MOTOYUKI
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APPLICANT:
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Patent No. 696299
GENERAL INFORMATION
APPLICANT: Pompedius, Markus
APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Hartwig
APPLICANT: Schoder, Oskar
APPLICANT: Haberhauer, Gregor
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING NOVEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Pompejus, Markus
APPLICANT: Kroger, Burkhard
APPLICANT: Schroder, Hartwig
APPLICANT: Zelder, Oskar
APPLICANT: Haberhauer, Gregor
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING NOVEL
TITLE OF INVENTION: PROTEINS
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40.0%; Pred. No. 45;
tive 3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              49.4%; Score 42; DB 2; Length 296; 40.0%; Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5; Indels
APPLICANT: NAGAHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
FILE REFERENCE: 084335/0160
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
FRIOR APPLICATION NUMBER: US/350,435
FRIOR FILING DATE: 2002-01-24
FRIOR RILING DATE: 2001-09-14
FRIOR PILING DATE: 2001-09-14
SOFTWARE: PATENTIN NUMBER: JP 2001-328381
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 3367
ILENGTH: 296
TYPE: PRT
CREATING APPLICATION NUMBER: 201
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 2367
ILENGTH: 296
TYPE: PRT
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CURRENT APPLICATION NUMBER: US/09/605,703B;
CURRENT FILING DATE: 2000-06-27
PRIOR APPLICATION NUMBER: 60/142,764
PRIOR FILING DATE: 1999-07-08
PRIOR FILING DATE: 1999-09-03
PRIOR FILING DATE: 1999-09-03;
NUMBER OF SEQ ID NOS: 2934
; SEQ ID NO 1364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 1364, Application US/09605703B; Patent No. 6962989; GENERAL INFORMATION:
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; ORGANISM: Corynebacterium glutamicum
US-09-605-703B-1364
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Matches 6; Conservative
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Best Local Similarity 40.0
Matches 6; Conservative
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US-09-605-703B-1364
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          FILE REFERENCE: BG1-129CP
CURRENT APPLICATION NUMBER: US/09/605,703B
CURRENT FILING DATE: 2000-06-27
PRIOR APPLICATION NUMBER: 60/142,764
PRIOR FILING DATE: 1999-07-08
PRIOR FILING DATE: 1999-09-03
PRIOR FILING DATE: 1999-09-03
PRIOR FILING DATE: 1999-09-03
LEWOTH: 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: August 30, 2006, 04:33:02
Job time : 15.8485 secs
                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-605-703B-1362
                                                                                                                                                                                                                                                                                                                                                                                               |:| |:| |:
185 HSDKPIRHEAELKGW 199
PROTEINS
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Best Local Similarity 40.01
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Sequence 184928, Sequence 38913, Sequence 38018, Sequence 32115, Sequence 23639, Sequence 3886, Ap Sequence 3886, Ap Sequence 320304, Sequence 220304, Sequence 220304, Sequence 2367, Ap Sequence 15, Appl Sequence 15, Appl Sequence 6449, Ap

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WS-09-479-614-14

Sequence 14, Application US/09479614

Publication No. US20030013183A1

Publication No. US20030013183A1

GENERAL INFORMATION:

APPLICANT: Wecall, Catherine

APPLICANT: Wecker, Eric

TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods

FILE REFERENCE: P-1047

CURRENT APPLICATION NUMBER: US/09/479,614

CURRENT PILING DATE: 1999-01-07

EARLIER FILING DATE: 1999-01-07

MUMBER: PATENTING DATE: 1999-01-07

NUMBER: PATENTING DATE: 2.0

SEQ ID NO 14

LENGTH: 431

TIPE: PRT

CORANISM: Felis Catus

US-09-479-614-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/10758165
Publication No. US20050196816A1
GENERAL INFORMATION:
APPLICANT HammerDay Bruce
1TILE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
FILE REFERENCE: 5051-661
CURRENT APPLICATION NUMBER: US/10/758,165
CURRENT FILING DATE: 2004-01-16
PRIOR PILING DATE: 2003-01-16
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin version 3.2
SEQ ID NO 2. APPLICATION OF SEQ ID NOS: 16
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 85; DB 5; Length 15;
Pred. No. 7e-08;
Mismatches 0; Indels
US-10-425-115-351700
US-10-425-115-184928
US-10-425-115-189173
US-10-425-114-38018
US-10-425-115-336115
US-10-425-115-33639
US-10-104-047-3886
US-10-1072-51-3886
US-10-25-115-20304
US-10-425-115-20304
US-10-425-115-220304
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ilarity 100.0%;
Conservative 0
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Best Local Similarity
Matches 15; Conserv
       US-10-758-165-2
          LENGTH: 15
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Sequence 13976, A
Sequence 13960, A
Sequence 9714, Ap
Sequence 145550,
Sequence 145550,
Sequence 283053,
Sequence 189170,
Sequence 189170,
Sequence 189170,
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Sequence 14, Appl
Sequence 14, Appl
Sequence 2, Appli
Sequence 29, Appl
Sequence 2, Appli
Sequence 29, Appli
Sequence 29, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 28, Appli
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320858,
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1. /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2. /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

3. /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

4. /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

5. /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

6. /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*
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                                                                                                                                                                           August 30, 2006, 04:33:28; Search time 75.7576 Seconds (without alignments) 91.717 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
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                                 GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-09-479-614-14

US-09-479-614-29

US-09-479-614-29

US-10-409-772-2

US-10-409-772-2

US-10-409-772-2

US-10-758-165-1

US-10-758-165-1

US-10-73-207-2

US-10-73-207-2

US-10-73-207-3

US-10-73-292-13976

US-10-732-923-13960

US-11-097-143-9714

US-09-924-841-8

US-10-93-13960

US-11-097-143-9714

US-09-924-841-8

US-10-92-115-19049

US-10-425-115-19049

US-10-425-115-18049

US-10-425-115-18049
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US-10-425-115-320858
US-10-329-433-115-320858
US-10-425-115-190842
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                               OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Match Length DB
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Minimum DB Maximum DB

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Result

Perfect score:

Run on:

Sequence:

Scoring table:

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Best Local Similarity 100.0
Matches 15; Conservative
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; ORGANISM: Felis catus
US-09-479-614-29
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; Sequence 14, Application No. US20030216565A1
; Bublication No. US20030216565A1
; GENERAL INPORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/10/409,772
; CURRENT FILING DATE: 2003-04-07
; PRIOR FILING DATE: 2000-01-07
; PRIOR FILING DATE: 2000-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
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Sequence 2, Application US/09479614

Publication No. US20030013183A1

GENERAL INFORMATION:
APPLICANT: McCall, Catherine
APPLICANT: WEBER, Eric
TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
FILE REFERENCE: P-1047

CURRENT APPLICATION NUMBER: US/09/479,614

CURRENT FILING DATE: 2000-01-07

EARLIER APPLICATION NUMBER: 60/115,033

EARLIER PILING DATE: 1999-01-07

SEALIER PILING DATE: 1999-01-07

SEALIER PILING DATE: 2.0

SEQ ID NOS: 34

SOFTWARE: Patentin Ver. 2.0
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100.0%; Score 85; DB 3; Length 431; 100.0%; Pred. No. 2.7e-06;
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100.0%; Pred. No. 3.2e-06;
                                        0; Mismatches
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Best Local Similarity 100.0
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Query Match 100.
Best Local Similarity 100.
Matches 15; Conservative
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ORGANISM: Felis catus
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ORGANISM: Felis catus
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Matches 15; Conserv
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US-10-409-772-14
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APPLICANT: McCall, Catherine
APPLICANT: Weber, Eric
TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
FILE REFERENCE: P-1047
CURRENT APPLICATION NUMBER: US/10/409,772
CURRENT APPLICATION NUMBER: US/09/479,614
PRIOR APPLICATION NUMBER: US/09/479,614
PRIOR FILING DATE: 2000-01-07
RUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 2.0
APPLICANT: McCall, Catherine
APPLICANT: Weber, Eric
TITLE OF INVENTION: Reline Immunoglobulin E Molecules and Related Methods
TITLE OF INVENTION: Reline Immunoglobulin E Molecules and Related Methods
FILE REPERENCE: P-1047
CURRENT FILING DATE: 1090-01-07
CURRENT FILING DATE: 1999-01-07
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PATENTIN VET: 2.0
SOFTWARE: PATENTIN VET: 2.0
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Pred. No. 3.2e-06;
; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                        Length 496;
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                                                                                                                                                                                                                                                                                                        100.0%; Score 85; DB 3; I 100.0%; Pred. No. 3.2e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Some Best Local Similarity 100.0%; Powatches 15; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                             427 HNDSPVRTEQOATTW 441
                                                                                                                                                                                                                                                                                                                                                                              1 HNDSPVRTEQQATTW 15
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US-10-214-524-25
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Sequence 2, Application US/10723207

| Publication No. US2005025034A1
| GENERAL INFORMATION:
| APPLICANT: Walfield, Alan M. |
| TITLE OF INVENTION: ALLERGY |
| FILE REPRENCE: 115.1-4153US2 |
| FRIOR APPLICATION NUMBER: 09/701, 623 |
| FRIOR FILING DATE: 1999-06-21 |
| FRIOR FILING DATE: 1999-06-21 |
| FRIOR APPLICATION NUMBER: 09/100, 287 |
| FRIOR APPLICATION NUMBER: 09/100, 287 |
| SOFTWARE: PALENTIN VET: 1988-06-20 |
| SOFTWARE: PALENTIN VET: 2.1 |
| SOFTWARE: PALENTIN VET: 1.1 |
| SEGION OF 2
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; Publication No. US20030073142A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Swey-Shen Alex
; APPLICANT: Yang, Yong-Min
; APPLICANT: Barankiewicz, Theresa J.
APPLICANT: Theorem Chen, Zhong
; TITLE OF INVENTION: IMMUNOCLOBULIN E VACCINES AND METHODS OF USE THEREOF
; FILE REFERENCE: IGE-00101.P.1.1
; CURRENT APPLICATION NUMBER: US/10/214,524
; CURRENT APPLICATION NUMBER: 60/312,120
; PRIOR FILING DATE: 2001-08-08
; PRIOR FILING DATE: 2001-08-13
; NUMBER: OF SEQ ID NOS: 61
; SEQ ID NO 28
; LENGTH: 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 48; DB 5; Length 312;
Pred. No. 7;
3; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Dog (Canis familiaris)
US-10-214-524-28
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61.5%;
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256 NDSPIQTDQYTTT 268
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JOURNAL: Immunogenetics
VOLUME: 41
PAGES: 282-286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PUBLICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 8; Conserv
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ORGANISM: Dog
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                                           JS-10-723-207-2
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US-10-723-207-2
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WS-10-409-772-29

Bublication UG/10409772

Publication No. US2030216565A1

Publication No. US2030216565A1

APPLICANT: Weber, Eric

TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods

FILE REFERENCE: P-1047

CURRENT FILING DATE: 2003-04-07

PRIOR FILING DATE: 2003-04-07

PRIOR FILING DATE: 2000-01-07

NUMBER OF SEQ ID NOS: 34

SOFTWARE: Patentin Ver. 2.0

LENGTH: 496
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Fublication No. US20050196816A1
GENERAL INFORMATION:
APPLICANT: Hammerberg, Bruce
TITLE OF INVENTION: IMMUNGLOBULIN E DETECTION IN MAMMALIAN SPECIES
FILE REFERENCE: 5051-661
CURRENT APPLICATION NUMBER: US/10/758,165
CURRENT PILING DATE: 2003-01-16
FRICH APPLICATION NUMBER: US 60/440,472
FRICH REPLICATION NUMBER: US 60/440,472
SEQ ID NOS: 16
SOFTWARE: PATENTIN VERSION 3.2
SEQ ID NOS: 16
SOFTWARE: PATENTIN VERSION 3.2
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                                                                                                                            100.0%; Score 85; DB 4; I
100.0%; Pred. No. 3.2e-06;
iive 0; Mismatches 0;
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100.0%; Pred. No. 3.2e-06;
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                                                                                                                            Query Match 100.
Best Local Similarity 100.
Matches 15, Conservative
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Best Local Similarity 100.
Matches 15; Conservative
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                                         ; TYPE: PRT
; ORGANISM: Felis catus
US-10-409-772-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Felis catus
US-10-409-772-29
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Best Local Similarity
Matches 8; Conservé
; SEQ ID NO 2
; LENGTH: 496
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Sequence 203123, Application US/10425115
; Sequence 203123, Application No. US20040214272A1
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Zhou, Yihua
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(5322)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 203123
; LENGTH: 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Cropbesign N.V.

TITLE OF INVENTION: Plant growth regulating genes, proteins and uses thereof
TITLE OF INVENTION: Plant growth regulating genes, proteins and uses thereof
FILE REFERENCE: CROP-028-PCT
CURRENT APPLICATION NUMBER: US/10/474,691
CURRENT FILING DATE: 2003-10-14
PRIOR FILING DATE: 2001-04-12
NUMBER OF SEQ ID NOS: 107
SOFTWARE: PatentIn version 3:1
SEQ ID NO 101
LENGTH: 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-732-923-13976

Sequence 13976, Application US/10732923

Publication No. US20050108791A1

GENERAL INFORMATION:

APPLICANT: Edgerton, Michael D

ATPLICANT: Edgerton, Michael D

TITLE OF INVENTION: TRANSCENIC PLANTS WITH IMPROVED PHENOTYPES

FILE REFERENCE: 38-115 (52796) C

CURRENT APPLICATION NUMBER: US/10/732,923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 47; DB 5; Length 84; Pred. No. 2.5; 3; Indels 2; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Clone ID: MRT4577_116836C.1.pep
US-10-425-115-203123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 47; D
Pred. No. 2;
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; Sequence 101, Application US/10474691
; Publication No. US20040221332A1
; GENERAL INFORMATION:
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Best Local Similarity 61.5%;
Matches 8; Conservative 7
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; ORGANISM: Gossypium arboreum
US-10-474-691-101
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32 NDSPAKTQSQGTT 44
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Best Local Similarity 69.2.
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ORGANISM: Zea mays
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; Sequence 13960, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION; Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-1567296)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT APPLICATION NUMBER: 10/310,154
; PRIOR APPLICATION NUMBER: 10/310,154
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 13960
; LEMOTH: 2360
; LEMOTH: 2360
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                                                                                                                                                                                                                Length 1083;
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                                                                                                                                                 , ORGANISM: Cryptococcus neoformans var. neoformans US-10-732-923-13976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 55.3%; Score 47; DB 5; Best Local Similarity 53.3%; Pred. No. 96; Matches 8; Conservative 0; Mismatches
                                                                                                                                                                                                                  5,
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US-10-732-923-13960
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Pred. No. 41;
O; Mismatches
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               PRIOR APPLICATION NUMBER: 10/310,154
PRIOR FILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 24149
SEQ ID NO 13976
LENGTH: 1083
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Best Local Similarity 53.3%;
Matches 8; Conservative (
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CURRENT FILING DATE:
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3513, Ap 16800, A 18766, A 255, App 23670, A 104477,

Sequence Sequence Sequence

115716, 104476, 115715, 64068, P 64067, P

Sequence Seq

Sequence Sequence Sequence

Perfect score:

Sequence:

OM protein -

Run on:

Scoring table:

Minimum DB Maximum DB

Database

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APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
ITLE REPRESENCE: MOA-A0205Y1-US
FULLS REPRESENCE: MOA-A0205Y1-US
CURRENT FLING DATE: 2003-05-29
PRIOR PLICATION NUMBER: UP 2002-203269
PRIOR APPLICATION NUMBER: UP 2002-2038870
PRIOR APPLICATION NUMBER: UP 2002-383870
PRIOR APPLICATION NUMBER: UP 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: Patentin Ver. 2.1
LENGTH: 980
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APPLICANT: National Institute of Physical Advancement Institution.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
IITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
FILE REPERBURE: MOA-A0205Y1-US
CURRENT APPLICATION UNMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
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                   US-11-330-403-3513

US-11-330-403-16800

US-11-330-403-16800

US-11-350-403-16800

US-11-056-355B-10470

US-11-056-355B-10470

US-11-056-355B-10470

US-11-056-355B-10470

US-11-056-355B-64069

US-11-056-355B-64069

US-11-056-355B-64069

US-11-056-355B-64069

US-11-056-355B-64069

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US-11-056-355B-64069
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US-11-350-703-1
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US-10-449-902-56184
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Publication No. US20060123505A1
GENERAL INFORMATION:
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Publication No. US20060123505A1
GENERAL INFORMATION:
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Best Local Similarity 46...
7; Conservative
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; ORGANISM: Oryza sativa
US-10-449-902-41347
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185, App
118, App
41297, A
34916, A
34916, A
1330, Ap
10350, A
10350, A
10350, A
36429, A
2561, A
104418,
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/EMC_Celerra_SIDS3/prodata/1/pubpaa/US06_NEW_PUB.pep:*
/EMC_Celerra_SIDS3/prodata/1/pubpaa/US07_NEW_PUB.pep:*
/EMC_Celerra_SIDS3/prodata/1/pubpaa/US08_NEW_PUB.pep:*
/EMC_Celerra_SIDS3/prodata/1/pubpaa/US08_NEW_PUB.pep:*
/EMC_Celerra_SIDS3/prodata/1/pubpaa/US06_NEW_PUB.pep:*
/EMC_Celerra_SIDS3/prodata/1/pubpaa/US16_NEW_PUB.pep:*
/EMC_Celerra_SIDS3/prodata/1/pubpaa/US16_NEW_PUB.pep:*
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                          GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-11-330-403-4388

US-11-330-403-5551

US-11-330-403-5751

US-11-330-403-1559

US-11-330-403-1559

US-11-330-403-1559

US-10-196-749-522

US-10-196-749-522

US-10-196-749-522

US-10-196-749-522

US-10-196-1859-165

US-10-196-1859-1897

US-11-056-3558-7331

US-11-056-3558-7331

US-11-056-3558-7339

US-11-056-3558-7339

US-11-056-3558-1059

US-11-056-3558-1039

US-11-056-3558-1039

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US-11-056-355B-104478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Published_Applications_AA_New:*
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                     protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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                                                                                                                                                                                                      Query Match 45.9%; Score 39; DB 6; Length 148; Best Local Similarity 46.7%; Pred. No. 17; Matches 7; Conservative 2; Mismatches 6; Indels
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Sequence 4388, Application US/11330403

Publication No. US20060159563A1

GENERAL INFORMATION:

APPLICANT: Abad, Mark S.

TITLE OF INVENTION: Genes and Uses for Plant Improvement

FILE REFERENCE: 38-21(53629)B

CURRENT APPLICATION NUMBER: US/11/330,403

CURRENT FILING DATE: 2006-01-12

NUMBER OF SEQ ID NOS: 19250

SEQ ID NO 4388

LENGTH: 151
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Pred. No. 26;
1; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Ludwig Institute for Cancer Research et al.
TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
FILE REFERENCE: 28967/39178
CURRENT APPLICATION NUMBER: US/10/505,928
CURRENT FILING DATE: 2004-08-27
FRIOR PELLORION NUMBER: US 60/363,019
FRIOR PELLON DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 866
SOFTWARE: Patentin 3.2
SEQ ID NO 255
LENGTH: 771
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: LOCATION: (1)..(151)

: OTHER INFORMATION: unsure at all Xaa locations

US-11-330-403-4388
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Pred. No. 97;
2; Mismatches
PRIOR FILING DATE: 2002-05-30
PRIOR PELIANG DATE: 2002-05-30
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SEQ ID NO 5: 56791
SEQ ID NO 51741
LENGTH: 148
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 255, Application US/10505928 Publication No. US20060088532A1 GENERAL INFORMATION:
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54.5%;
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Best Local Similarity 63.6%;
Matches 7; Conservative
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Best Local Similarity 54.5.
6; Conservative
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                                                                                                                                ; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-51741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-255
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ORGANISM: Zea mays
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44.7%; Score 38; DB 7; Length 153;
Best Local Similarity 63.6%; Pred. No. 27;
Matches 7; Conservative 1; Mismatches 3; Indels
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; Publication No. US20060159563A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFRENCE: 38-21 (53629) B
; CURRENT APPLICATION NUMBER: US/11/330,403
; CURRENT FILING DATE: 2006-01-12
; NUMBER OF SEQ ID NOS: 19250
; SEQ ID NO 4345
; LENGTH: 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 156;
                                                                                                                                                                   US-11-330-403-5751
; Sequence 5751, Application US/11330403
; Publication No. US20060159563A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(55629)B
; CURRENT APPLICATION UNMERF: US/11/330,403
; CURRENT FILING DATE: 2006-01-12
; NUMBER OF SEQ ID NOS: 19250
; SEQ ID NO S: 551
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Sequence 7573
Sequence 7573
Sequence 7573
Publication No. US20660159563A1
Septence 7574
Septence 7574
Septence 7575
Septence 757
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Pred. No. 27;
1; Mismatches
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CTHER INFORMATION: unsure at all Xaa locations US-11-330-403-5751
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ilarity 63.6%;
Conservative
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54 NDPPVRNSQEA 64
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Best Local Similarity
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Publication No. US20060123505A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: National Institute of Agrobiological Sciences.

APPLICANT: Bid-oritanted Technology Research Advancement Institution.

APPLICANT: The Institute of Physical and Chemical Research.

APPLICANT: Foundation for Advancement of International Science.

TITLE OF INVENTION: FULL-LENGITH PLANT CDNA AND USES THEREOF

FILE REFERENCE: MOA-A0205Y1-US

CURRENT FILING DATE: 2003-05-29

PRIOR APPLICATION NUMBER: UP 2002-203269

PRIOR APPLICATION NUMBER: UP 2002-383870

PRIOR PILING DATE: 2002-12-11

NUMBER OF SEQ ID NOS: 56791

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 37829

LENGTH: 436
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                                                                                                                                                                                                                                                                                                                                                                                    US-11-330-403-12509

Sequence 12509, Application US/11330403

Publication No. US20060159563A1

GENERAL INFORMATION:
TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REFERENCE: 38-21(53629)B

CURRENT APPLICATION NUMBER: US/11/330,403

CURRENT FILING DATE: 2006-01-12

NUMBER OF SEQ ID NOS: 19250

LENGTH: 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 38; DB 7; Length 242; Pred. No. 43; 1; Mismatches 3; Indels
                                                                                                                                                                                                                                  3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; LOCATION: (1)..(242)
; OTHER INFORMATION: unsure at all Xaa locations US-11-330-403-12509
                                                                                             NAME/KEY: unsure

: LOCATION: (1)..(174)

: OTHER INFORMATION: unsure at all Xaa locations
US-11-330-403-7573
                                                                                                                                                                                              44.7%;
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63.6%;
                                        TYPE: PRT
ORGANISM: Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                        Query Match
Best Local Similarity 63.6
Matches 7; Conservative
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; ORGANISM: Oryza sativa
US-10-449-902-37829
SEQ ID NO 7573
LENGTH: 174
                                                                              FEATURE:
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APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

TITLE OF INVENTION: ACIDS ENCODING THE SAME

FILE REPERBUCE: P3430R1C340

CURRENT FILING DATE: 2002-07-16

PRIOR PPLICATION NUMBER: 10/052586

PRIOR APPLICATION NUMBER: 10/05266

PRIOR APPLICATION NUMBER: 60/059266

PRIOR PLING DATE: 1997-09-18

PRIOR PLING DATE: 1997-09-18

PRIOR PLING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/063250

PRIOR PLING DATE: 1997-10-24

PRIOR PLING DATE: 1997-10-28

PRIOR PRIOR PRIOR DATE: 1997-10-28

PRIOR PRIOR PR
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Pred. No. 97;
3; Mismatches 6; Indels
DB 6; Length 436;
80;
                                                                           3; Mismatches
Score 38;
Pred. No.
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i, Sequence 165, Application US/10700439

i, Publication No. US20060188889A1

i, GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 522, Application US/10196749
Publication No. US20060094864A1
GENERAL INFORMATION:
44.78;
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40.0%;
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                                                                                                                                                      1 HNDSPVRTEQOATTW 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gurney, Austin L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Baker, Kevin P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo Sapien
US-10-196-749-522
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Best Local Similarity
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TYPE: prt
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APPLICANT: Burgart, Lawrence
APPLICANT: Boardman, Lisq A.
APPLICANT: Boardman, Lisq A.
APPLICANT: Thibodeau, Steven
APPLICANT: Thibodeau, Steven
APPLICANT: Lewis, Marcia
TITLE OF INVENTION: Use of Differentially Expressed Nucleic Acid Sequences as
TITLE OF INVENTION: Biomarkers for Cancer
FILE REFERENCE: 1657/2022
CURRENT APPLICATION NUMBER: US/10/700,439
NUMBER OF SEQ ID NOS: 186
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NOS: 186
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APPLICANT: Bio-oriented Technology Research Advancement Institution.
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Publication No. US20060121561A1

GENERAL INFORMATION:

APPLICANT: Fritach Olivier

APPLICANT: Hoth Barbara

APPLICANT: Lucht Jan Martin

TILLE OF INVENTION GENE FOR INCREASED SOMATIC RECOMBINATION

FILE REPERENCE: 1-3246B/FM1

CURRENT APPLICATION NUMBER: US/10/519,069

CURRENT APPLICATION NUMBER: US/10/519,069

CURRENT APPLICATION NUMBER: PCT/RE03/006757

PRIOR PILING DATE: 2003-06-26

PRIOR PILING DATE: 2003-06-26

PRIOR FILING DATE: 2003-06-26

PRIOR PLING DATE: 2003-06-26

PRIOR FILING DATE: 2003-06-27

NUMBER OF SEQ ID NOS: 30

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 18

LENGTH: 596
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Mayo Foundation for Medical Education and Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44.7%; Score 38; DB 6; Length 530; 40.0%; Pred. No. 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Indels
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; Publication No. US20060123505A1
; GENERAL INFORMATION:
                   Bayer Healthcare LLC
Burgess, Christopher
Myerow, Susan
Thiagalingam, Arunthathi
Maimonis, Peter
Molino, Gary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Arabidopsis thaliana US-10-519-069-18
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450 HHDQPVKPLDRAVFW 464
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Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 13
US-10-449-902-41297
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US-10-519-069-18
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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US-10-953-349-34917
Sequence 34917, Application US/10953349
Sequence 34917, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: ENCONDED THERBY
TITLE OF INVENTION: ENCONDED THERBY
FILE REPERBERCE: 2750-1579FUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 34917
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; Sequence 7331, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REPERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR RILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 7331
LENGTH: 132
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APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
ITILE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
FILE REFERENCE: MONA-AO20571-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT APPLICATION NUMBER: US 2002-203269
PRIOR PILING DATE: 2002-05-39
PRIOR PILING DATE: 2002-05-30
PRIOR PILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTHARE: PARTENTIN VET: 2.1
SEQ ID NO 41297
LENGTH: 1093
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Pred. No. 2.1e+02;
3; Mismatches 4;
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44.1%; Score 37.5; D

Best Local Similarity 53.3%; Pred. No. 28;

Matches 8; Conservative 2; Mismatches
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US-10-953-349-34917
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illarity 50.0%;
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98 HRESPSRPPRQATS 111
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                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Oryza sativa
US-10-449-902-41297
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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44.1%; Score 37.5; DB 7; Length 132;
Best Local Similarity 53.3%; Pred. No. 28;
Matches 8; Conservative 2; Mismatches 4; Indels 1
; ORCANISM: Zea mays subsp. mays; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1). (13.2)
; OTHER INFORMATION: Ceres Seq. ID no. 13498699
US-11-056-3558-7331
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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RNNVLIQTDQQATTR 15 US-10-758-165A-3 Perfect score: Sequence: Title:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2589679 seqs, 457216429 residues Searched:

2589679 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2006s:* geneseqp1980s:* geneseqp2005s:* A_Geneseq_8:* 1: geneseqp198 2: geneseqp199 •• Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STEMMARTES

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Result	2000	Query	Query	ä	£	2000
. :	1000	Maccai	nenden.	9 !	4	Description
1	74	100.0	15	œ	ADR10603	Adr10603 Horse IgE
7	74	100.0	424	'n	AAM50103	Aam50103 Equine Ig
m	74	100.0	424	S	AAM50104	Aam50104 Equine Ig
4	74	100.0	266	σ	AED15438	Aed15438 Equine Pr
2	74	100.0	266	10	AEE88000	Aee88000 Human pro
9	74	100.0	569	9	ABP96585	Abp96585 Horse IgE
7	49	66.2	15	7	ADC64568	
œ	43	58.1	417	σ	AEB39722	Aeb39722 L. pneumo
σ	43	58.1	452	σ	AEB36305	Aeb36305 L. pneumo
10	43	58.1	580	Ŋ	ABG32001	ä
11	43	58.1	580	œ	ADP79623	Adp79623 Giardia i
12	41	55.4	15	œ	ADR10601	
13	41	55.4	312	ო	AAY79995	Aay79995 Dog immun
14	41	55.4	312.	ω	ADN24060	Adn24060 Bacterial
15	41	55.4	417	7	AAW23067	Aaw23067 Canine Ig
16	41	55.4	426	7	AAR97753	Aar97753 Canine Ig
17	41	55.4	426	9	ABP96583	Abp96583 Dog IgE h
18	41	55.4	2000	Q	ABR52669	
19	41	55.4	2000	7	ADK61774	Adk61774 Disease t
20	40	54.1	15	œ	ADR10607	Adr10607 Pig IgE e
21	40	54.1	567	9	ABP96588	
22	38	51.4	613	N	AAW73009	Aaw73009 Cobra ven
23	38	51.4	621	7	AAW73013	Aaw73013 Cobra ven

Aspergill	Glycoside	Cat IgE e	Propionib	Propionib	Oil-assoc	ZooA prot	Acinetoba	Cat immun	Cat IgE h	Feline Ig	Feline Ig	Cat parti	Cat parti	Oil-assoc	Propionib	Propionib	Peptide f	Streptoco	Streptoco	Aspergill
Abj26042	Aec10425	Adr10602	Aau62291	Abm58810	Adj48583	Aay17498	Ada34539	Adg73237	Abp96580	Abu09338	Abu09336	Adg73251	Adg73225	Adj 49049	Aau48101	Abm44620	Adm66490	Adv87747	Adv79000	Ab 126246
ABJ26042	AEC10425	ADR10602	AAU62291	ABM58810	ADJ48583	AAY17498	ADA34539	ADG73237	ABP96580	ABU09338	ABU09336	ADG73251	ADG73225	ADJ49049	AAU48101	ABM44620	ADM66490	ADV87747	ADV79000	ABJ26246
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51.4	51.4	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	48.6	48.6	48.6	48.6
38	38	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	36	36	36	36
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50.0 496 8 ADG4949 Adg73225 9 37 50.0 49

ALIGNMENTS

Horse IgE epitope recognised by monoclonal antibody 5.91, SEQ ID 3. ADR10603 standard; peptide; 15.AA. 21-OCT-2004 (first entry) ADR10603; RESULT 1 ADR10603 ID ADR1

Antiasthmatic, Antiallergic, Immunosuppressive, IgE; dog; asthma; anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody; Equus caballus. horse.

WO2004065936-A2.

05-AUG-2004.

15-JAN-2004; 2004WO-US003566.

16-JAN-2003; 2003US-0440472P.

(UYNC-) UNIV NORTH CAROLINA STATE.

Hammerberg B;

WPI; 2004-593545/57.

Novel antibody that specifically binds to mammalian IgE epitope, useful for testing an allergen reactivity of IgE sample, detecting mammalian IgE or treating asthma or anaphylactic shock.

Example 6; Page 9; 14pp; English.

The present invention relates to a novel monoclonal antibody (1) that specifically binds to a mammalian IgE epitope, where the epitope is between amino acids 145-166 or 156-374 of mammalian IgE, e.g. dog IgE. (1) is useful for testing an allergen reactivity of an IgE sample. The allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut and corn allergens. The sample is a biological sample collected from a dog, cat or horse. (1) is also useful for detecting mammalian IgE and for treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal antibodies recognise epitopes on canine IgE corresponding to amino acid residues 357-371 (ADR10601) and 146-162 (ADR10609) respectively of the

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention describes a novel DNA (I) encoding the constant region (CH) of the heavy chain of a horse immunoglobulin E (IgE) allotype. The products of the invention are capable of neutralising IgE activity and have antiallergic activity. The polyuncleotides of the invention are used to produce recombinant IgE (II), and this is used to raise specific monoclonal antibodies (MAb). Both (II) and MAb are useful for diagnosis, particularly of allergy in horses, and MAb can also be used for treatment of allergies. (I) make possible production of isotype-specific antibodies, important for precise evaluation of the immune response. This
cannne IgE epsilon-chain. Recognition of epsilon-chains from IgE from cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and 3.76 were observed to have good cross-reactivity with the epsilon-chain of IgE from cat and horse, but did not exhibit cross-reactivity with either pig or human epsilon-chains of IgE. The present sequence is the horse IgE 5.91 recognition site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence encoding part of an equine immunoglobulin G, useful for paring isotype-specific antibodies for diagnosis and treatment of
                                                                                                                                                                                 Gaps
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                                                                                                                                                  100.0%; Score 74; DB 8; Length 15;
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Mismatches 0;
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/note= "CH1 domain"
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206. .312
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/note= "CH4 domain"
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Best Local Similarity 100.
Matches 15; Conservative
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                                                                                                                      Sequence 15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Equus caballus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention describes a novel DNA (I) encoding the constant region (CH) of the heavy chain of a horse immunoglobulin E (IgE) allotype. The products of the invention are capable of neutralising IgE activity and have antiallergic activity. The polymucleotides of the invention are used to produce recombinant IgE (II), and this is used to raise specific monoclonal antibodies (MAD). Both (II) and MAD can also be used for diagnosis, particularly of allergy in horses, and MAD can also be used for treatment of allergies. (I) make possible production of isotype-specific antibodies, important for precise evaluation of the immune response. This sequence represents a fragment of the equine IgE heavy chain constant region C-epsilon allotype b (Ceb), used in the method of the invention for IgE-isotype recombinant immunoglobulin production
sequence represents a fragment of the equine IgE heavy chain constant region C-epsilon allotype a (Cea), used in the method of the invention for IgE-isotype recombinant immunoglobulin production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA sequence encoding part of an equine immunoglobulin G, useful for preparing isotype-specific antibodies for diagnosis and treatment of allergy in horses.
                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                            Ceb; equine; horse; heavy chain; constant region; allotype b; IgE; C-epsilon b; immunoglobulin E; antiallergic; allergy.
                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                             Equine IgE heavy chain constant region C-epsilon allotype b.
                                                                                              Length 424;
                                                                                                                           Indels
                                                                                            Score 74; DB 5; I
Pred. No. 8.6e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TIER-) TIERAERZTLICHE HOCHSCHULE HANNOVER.
                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .9/
/note= "CH1 domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98. .205
/note= "CH2 domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "CH3 domain"
                                                                                                                                                                                                                                                                     AAM50104 standard; protein; 424 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "CH4 domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 34-36; 37pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Radbruch A;
                                                                                                                             ;
0
                                                                                               100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-DEC-2001; 2001WO-DE004810.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-DEC-2000; 2000DE-01064415.
                                                                                                            100.0%;
                                                                                                                                                                             RNNVLIQTDQQATTR 370
                                                                                                                                                            1 RNNVLIQTDQQATTR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .424
                                                                                                                                                                                                                                                                                                                                 02-SEP-2002 (first entry)
                                                                                                           Local Similarity 100.
ses 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wagner B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-508803/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; ABL61247
                                                                 Sequence 424 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Equus caballus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200250280-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Leibold W,
                                                                                                                                                                                                                                                                                                    AAM50104;
                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Key
Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Domain
                                                                                                                Best Loc
Matches
                                                                                                                                                                                                                                                        AAM50104
                                                                                                                                                                                                                                      RESULT
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New isolated Equine Protozoal Myeloencephalitis (EPM) marker polynucleotides and polypeptides, useful in diagnosing, monitoring and treating EPM in affected animals, e.g. horse.
                                    Gaps
                                                                                                                                                                      Equine Protozoal Myeloencephalitis marker polypeptide, SEQ ID No:21.
                                   ö
                                                                                                                                                                                        equine protozoal myeloencephalitis; genetic marker; diagnosis; sarcocystis neurona infection; protozoacide.
                   Length 424;
                 Score 74; DB 5; Length 42.
Pred. No. 8.6e-05;
Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                              (GENO-) GENOMICS RES PARTNERS PTY LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 21; 356pp; English
                                                                                                                 AED15438 standard; protein; 566 AA.
            100.0%; Sco
100.0%; Pre
                                                                                                                                                                                                                                                                                          19-MAR-2004; 2004AU-00901448.
29-MAR-2004; 2004US-0556869P.
23-JUN-2004; 2004US-0581840P.
                                                              356 RNNVLIQTDQQATTR 370
                                                                                                                                                                                                                                                                         21-MAR-2005; 2005WO-AU000401
                                                   1 RNNVLIQTDQQATTR 15
                                                                                                                                                    (first entry)
                          Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                Brandon RB, Thomas MR;
                                                                                                                                                                                                                                                                                                                                                                  WPI; 2005-659146/67.
Sequence 424 AA;
                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AED15437
                                                                                                                                                                                                                                    WO2005090593-A1.
                                                                                                                                                    01-DEC-2005
                                                                                                                                                                                                                                                       29-SEP-2005
                                                                                                                                   AED15438;
                 Query Match
                                                                                                       RESULT
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The invention relates to isolated Equine Protozoal Myeloencephalitis

(EPM) marker polynucleotide sequences selected from any of the fully
defined sequences (SEQ ID Nos 1, 3, 5, 7, 8, 10, 12, 14, 16, 17, 18, 20,
22, 24, 26, 27, 28, 30, 33.4-50, 52, 54, 55, 56, 57, or 422) in the
Specification. The EPM polynucleotide sequences encode EPM polypeptides
(SEQ ID Nos 2, 4, 6, 9, 11, 13, 15, 19, 21, 23, 25, 29, 31, 33, 51, 53,
or 58). Also described are: (1) a method of diagnosing the presence of
EPM or Sarcocystis neurona infection in a test subject; (2) a method of
treating, preventing, or inhibiting the development of EPM in a subject;
(3) a nucleic acid construct comprising an EPM marker polynucleotide in
operable connection with a regulatory element that is operable in a host
cell; (4) an isolated host cell containing the nucleotide sequence that
hybridizes under low stringency conditions to the polynucleotide; and (6)
a solid or semi-solid support comprising a nucleotide sequence that
hybridizes under low stringency conditions to the polynucleotide; and
a solid or semi-solid support comprising a least one probe immobilized
or it. The EPM marker polynucleotides, probes, EPM marker polypeptides,
or antigen-binding molecules that are immuno-interactive with the EPM
marker polypeptide, are useful for diagnosing the presence of EPM in a
cubject. The EPM marker polynucleotides and polypeptides are also useful
for the diagnosis, monitoring, and treatment of EPM in affected animals.
This sequence represents an EPM marker polypeptide.
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Sequence 566 AA;

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The invention relates to a method of determining the presence or degree of a physiological response to stress or a related condition in a test subject comprising detecting in the test subject aberrant expression of at least one stress marker gene given in the specification. The invention also relates to a method of treating, preventing or inhibiting the development of stress in a subject, an isolated stress marker polymucleotide, a mucleic acid construct comprising a stress marker polymucleotide in operable connection with a regulatory element that is polymucleotide in operable connection with a regulatory element that is coprable in a host cell, an isolated host cell containing the construct, a probe comprising a nucleotide sequence that hybridizes under a least construction appoint comprising at least one probe immobilized on it. The stress marker polymucleotides, probes, stress marker polymeliaes, probes, stress marker polymeliaes, probes, stress marker polymeliaes, probes, stress marker polymeliaes, probes, stress mannfacture of a kit for diagnosing the presence of a physiological response to stress in a subject. The methods are useful for the mannfacture of a kit for diagnosing the presence of a physiological response to stress in a subject. The physiological response to stress is selected from physical stress, mood disorders, anxiety disorders, inflammation, pain, chronic fatigue syndrome, stress in immunodeficiency virus (filty) infections, neurodegenerative diseases, amyotrophic lateral sclerosis, a decrease in immunosubpression, hemorragic stress, stress, stress induced headache, cancer, human immunosuppression, hemorragic stress, stress, stress in immunosubpression, hemorragic stress, stress, stress in immunosubpression, endergene of immunosupression, hemorragic stress, stress, stress induced to immunosuppression, hemorragic stress, stress, stress induced between the immunosuppression, hemorragic stress, stress, stress, stress induced to manner in immunosuppression, entergates of immunosuppression, he
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Determining presence or degree of a physiological response to stress related condition in a test subject, comprises detecting in the test subject aberrant expression of at least one stress marker gene.
                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                          Diagnosis; immunity; stress; psychiatric disorder; tranquilizer.
                                                               .;
0
                        Length 566;
  Score 74; DB 9; Length bor
Pred. No. 0.00012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 136; 445pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GENO-) GENOMICS RES PARTNERS PTY LTD.
                                                                                                                                                                                                                                                    AEE88000 standard; protein; 566 AA.
                                                               0;
                      100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-JUN-2005; 2005WO-AU000794.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-JUN-2004; 2004US-0576285P.
                                                                                                                                               RNNVLIQTDQQATTR 513
                                                                                                     1 RNNVLIQTDQQATTR 15
                                                                                                                                                                                                                                                                                                                                                                                Human protein sequence #49
                                                                                                                                                                                                                                                                                                                                      23-FEB-2006 . (first entry)
                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thomas MR;
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2006-039470/04.
N-PSDB; AEE87999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO2005118810-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brandon RB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-DEC-2005
                                                                                                                                                                                                                                                                                              AEE88000;
                                                                                                                                                                                                             RESULT 5
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elicit in a mammal a CTL response to naturally processed and presented 1gE peptides. C1-3 have antiallergic, antiasthmatic, immunosuppressive, vasotropic, dermatological, antiinflammatory and cytostatic activities, and can be used as inducers of a CTL response against 1gE, and in vaccines. C1-3 can be used for modulating an IgE-mediated condition in a mammal. C1-3 are useful for modulating an IgE-mediated condition such as IgE-mediated atopic hypersensitivity condition, IgE-mediated condition auseful for treating atopic hypersensitivity condition, IgE-mediated non-atopic useful for treating atopic hypersensitivity conditions (such as allergic rhinitis, allergic asthma, food allergies, or atopic dermatitis), non-atopic hypersensitivity conditions (such as anaphylaxis, and urticaria hives). The present sequence represents an IgE heavy chain amino acid sequence, which is given in an example from the present invention

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(ADH), overeating or obesity, infertility, head traumas, spinal cord trauma, ischemic neuronal damage, excitotoxic neuronal damage, epilepsy, cardiovascular diseases, stroke, immune dyfatnotions, muscular spaems, urinary incontinence, senile dementia, Alzheimer's disease, multi-infarct dementia, amyotrophic lateral sclerosis, chemical dependencies and addictions, drug and alcohol withdrawal symptoms, osteoporosis, psychosocial dwarfism, hypoglycemia, hair loss, abnormal circadian rhythm or disorders related to abnormal circadian rhythm. This sequence represents a human protein used in the method of the invention.
                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                    Length 566;
                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                    Score 74; DB 10;
Pred. No. 0.00012;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                ABP96585 standard; protein; 569 AA.
                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                    100.0%;
                                                                                                                                                                                                                                                                                                                                 499 RNNVLIQTDQQATTR 513
                                                                                                                                                                                                                                                                                                                15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                1 RNNVLIQTDOOATTR
                                                                                                                                                                                                                  Ouery Match
Best Local Similarity
                                                                                                                                                                                                  Sequence 566 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABP96585;
                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 6
             888888888888888
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Gaps

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Length 569; Indels

100.0%; Score 74; DB 6; I 100.0%; Pred. No. 0.00012; Mismatches

. 0

Conservative

Best Local Similarity Matches 15; Conserv

Query Match

Sequence 569 AA;

1 RNNVLIQTDOOATTR 15

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Identifying peptides that induce cytotoxic T-lymphocyte, CTL response against 1gE, by identifying peptide eliciting CTL response to 1gE peptides naturally presented by major histocompatibility complex class I Immunoglobulin B; vaccine; IgE; cytotoxic T lymphocyte response; immune response; antiallargic; antiasthmatic; immunosupressive; vasctropic; cytostatic; dermatological; antiinflammatory; IgE-mediated condition; food allergy; atopic hypersenaitivity condition; allergic atipic dermatilis; non-atopic hypersensitivity non-atopic hypersensitivity condition; allergic asthma; atopic dermatitis; non-atopic hypersensitivity condition; anaphylaxis; Horse IgE heavy chain amino acid sequence SEQ ID NO:30. Chen Yang Y, Barankiewicz T, 13-AUG-2001; 2001US-0312120P. 08-AUG-2002; 2002WO-US026986 (IGET-) IGE THERAPEUTICS INC WPI; 2003-268242/26 WO2003015716-A2. urticaria hives Equus caballus. 27-FEB-2003. Chen SA, ABP96585

IID ABP9

XX ABP9

XX ABP9

XX ABP9

XX ABP9

XX Immu

I

The present invention describes a method (MI) for identifying peptides that induce cytotoxic T-lymphocyte (CTL) response against immunoglobulin B (IgB), comprising providing a test peptide (T) suspected of being able to bind to major histocompatibility complex (MHC) class I molecule, and evaluating (T) for ability to elicit in a mammal a CTL response to induces such a response is identified. Also described are compositions: (C1) comprising at least one immunogenic peptide (I) identified by (MI); (C2) comprising at least one isolated polynuclectide encoding (I); and (C3) comprising antigen-presenting cells that recognise at least one (I) where C1-3 are able to bind to at least one MHC class I molecule and to

Example 7; Page 157-160; 187pp; English

protein

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The invention relates to an immunogenic composition comprising an isolated polypeptide having an amino acid sequence that is at least 80% identical to 6 (81-86), 15 amino acid peptide sequences derived from antibody that specifically binds to equine immunoglobulin E (the composition induces production of an antibody that specifically binds to equine immunoglobulin (Ig)E), the six polypeptides are not explicitly identified in the specification. Also included are a composition comprising an antibody that specifically binds to a polypeptide at least 80% identical to (S1)-(S6), an antibody that specifically binds to equine IgE made by the process of immunising an antibody that specifically binds to equine IgE (involving immunising an antibody that specifically binds to equine IgE (involving immunising an antibody confirm of further comprising an isolated polypeptide (the animal with a composition further comprising an isolated polypeptide (the animal with a definition of the polypeptide is at least 80% identical to (S1)-(S6)), and collecting antiserum from the animal) and a kit for detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Immunogenic composition comprising an isolated equine immunoglobulin E polypeptide that induces production of antibodies which specifically bind to equine immunoglobulin E.
                                                                                                                                                                                                                                      Horse immunoglobulin E, IgE, heavy chain immunogenic peptide P4.
                                                                                                                                                                                                                                                                            Horse; immunoglobulin B; IgE; heavy chain; immunogen; allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kalina WV;
                                                                                                                    ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 8; 14pp; English.
                                                                                                                    ADC64568 standard; peptide; 15
                                                                                                                                                                                                                                                                                                                                                                                                                                            08-NOV-2001; 2001US-00052788.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-NOV-2001; 2001US-00052788
Gershwin LJ, Pettigrew HD,
                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-765437/72.
                                                                                                                                                                                                                                                                                                                                                              US2003087314-A1
                                                                                                                                                                                                                                                                                                                        Squus caballus.
                                                                                                                                                                                                18-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                      08-MAY-2003
                                                                                                                                                            ADC64568;
                                                                                                 ADC64568
                                                                           RESULT
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for detecting specific binding of the antibody to equine ISE. The antibody is useful for detecting equine ISE protein in a biological sample (serum) which involves contacting the sample with the antibody thus forming an antigen/antibody complex, and detecting the presence or absence of the antigen/antibody complex, the antibody and antigen are immobblised on a solid surface. The antibody is labelled such that the complex can be detected. The complex is detected using a second labelled antibody. The peptides are useful for generating antibodies specific for ISE which can serve as a diagnostic test for allergy. The present sequence is a Horse immunoglobulin B, ISE, heavy chain immunogenic peptide from the early portion of the C4 region.
equine IgE in a biological sample comprising the antibody and means
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Sequence 15 AA;

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                              Gaps
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        Score 49; DB 7; Length 15;
Pred. No. 0.074;
                             0; Indels
                             Mismatches
66.2%; Sco.
100.0%; Pred
0; N
                           10; Conservative
      Query Match
Best Local Similarity
                            Matches
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AEB39722 standard; protein; 417 AA (first entry) 08-SEP-2005 AEB39722;

L. pneumophila protein SEQ ID NO 4054

detection; infection; Antibacterial; Vaccine.

Legionella pneumophila.

WO2005049642-A2.

23-SEP-2004; 2004WO-IB003578. 02-JUN-2005.

21-NOV-2003; 2003FR-00013687.

(INSP) INST (INRM) INSER

Etienne J, Ma L, Cazalet C, Zidane N, Magnier A, Kunst F, (INSP) INST PASTEUR. (INRM) INSERM INST NAT SANTE & RECH MEDICALE. (INRY-) UNIV LYON I BERNARD CLAUDE. (CNRS) CNRS CENT NAT RECH SCI. C, Tichit M, Bouchier C, Buchrieser C, Rusniok C, Bo Jarraud S;

WPI; 2005-388305/40.

genome of Legionella pneumophila Paris strain and derived ypeptides, useful for detection or identification of the strain and treatment and prevention of infections. polypeptides, New for

Claim 3; SEQ ID NO 4054; 660pp; English.

The invention relates to an isolated or purified nucleotide sequences (I) from Legionella pneumophila Paris strain. (I), and their related sequences or fragmence, are useful as primers and probes for detection and amplification, including differentiation between the Paris and Philadelphia strains of Legionella pneumophila and to prepare recombinant (hybrid) polypeptides (II). (II) are also useful for preparation of specific antibodies (Ab), also used for detection/identification of Legionella, and some (I), specifically those involved in synthesis of surface proteins, are targets for identification of inhibitors. (II), or vectors that contain (I), are useful as vaccines and immunogenic

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             pneumophila. The present squence represents the amino acid sequence of a {\bf L}. pneumophila protein.
                                                                                                         Gaps
                                                                                                         .;
0
compositions, for treatment and prevention of infections by L.
                                                                              Length 417;
                                                                               6
                                                                              Score 43; DB 9
Pred. No. 38;
1; Mismatches
                                                                              58.1%;
69.2%;
                                                                Query Match
Best Local Similarity 69.27
Best Local 9; Conservative
                                                    Sequence 417 AA;
883333
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2 NNVLIQTDQQATT 14 63 NNVLIPLEQOPTT 75 셤 à

AEB36305 standard; protein; 452 AA. AEB36305

RESULT

AEB36305;

(first entry) 08-SEP-2005 L. pneumophila protein SEQ ID NO 637

detection; infection; Antibacterial; Vaccine.

Legionella pneumophila.

WO2005049642-A2.

32-JUN-2005

23-SEP-2004; 2004WO-IB003578

21-NOV-2003; 2003FR-00013687

(INSP) INST PASTEUR.

INSERM INST NAT SANTE & RECH MEDICALE. UNIV LYON 1 BERNARD CLAUDE. CNRS CENT NAT RECH SCI. (INRM) (UYLY-)

(CNRS)

Vandenesch F; Glaser P; , Ma L, Cazalet C, Magnier A, Kunst F, Etienne J, Zidane N, Tichit M, Bouchier C, Buchrieser C, Rusniok C, Jarraud S;

WPI; 2005-388305/40.

New genome of Legionella pneumophila Paris strain and derived polypeptides, useful for detection or identification of the strain and for treatment and prevention of infections.

Claim 3; SEQ ID NO 637; 660pp; English.

Glaser P; Vandenesch F;

The invention relates to an isolated or purified nucleotide sequences (I) from Legionella pneumophila Paris strain. (I), and their related sequences or fragments, are useful as primers and probes for detection and amplification, including differentiation between the Paris and Philadelphia strains of Legionella pneumophila and to prepare recombinant (hybrid) polypeptides (II) (II) are also useful for preparation of Legionella, and some (I), specifically those involved in synthesis of surface proteins, are targets for identification of inhibitors. (II), or vectors that contain (I), are useful as vaccines and immunogenic compositions, for treatment and prevention of infections by L. pneumophila. The present squence represents the amino acid sequence of a L. pneumophila protein.

Sequence 452 AA;

ö Gaps ; 0 Length 452; 3; Indels DB 9; 1; Mismatches Score 43; Pred. No. 58.1%; Conservative Best Local Similarity Matches 9; Conserv Query Match

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Arginine deaminase; cytostatic; virucide; viral replication; nitric oxide synthesis; tumour; liver function; enzyme.
                                                                                                                        Giardia intestinalis arginine deaminase.
                                                                                                                                                                                                                                                                                                                                                             (PHOE-) PHOENIX PHARMACOLOGICS INC.
                              ADP79623 standard; protein; 580 AA.
                                                                                                                                                                                                                                                                                                  29-SEP-2003; 2003WO-US030770.
                                                                                                                                                                                                                                                                                                                              18-NOV-2002; 2002US-0427497P.
                                                                                            04-NOV-2004 (first entry)
                                                                                                                                                                                                      Giardia intestinalis.
                                                                                                                                                                                                                                   WO2004046309-A2
                                                                                                                                                                                                                                                                   03-JUN-2004
                                                                                                                                                                                                                                                                                                                                                                                            Clark MA;
                                                             ADP79623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 12
RESULT 11
                 ADP79623
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention discloses a compound comprising arginine deiminase (ADI)

covalently bonded by a linking group to polyethylene glycol (PEG) having

a total weight average molecular weight of about 1000-50000. Also

disclosed is a method for enhancing the circulating half life or the

tumouricidal activity of arginine deiminase by modifying the arginine

deiminase by covalently bonding the arginine faciminase by a linking group

to PEG. Normal cells can synthesise arginine from circulline in a 2 step

process catalysed by argininosuccinate synthase and argininosuccinate

lyase. In contrast, many cancerous cells do not express argininosuccinate

synthase and are, therefore, auxotrophic for arginine. Arginine deiminase

catalyses the conversion of arginine to circulline and be used to

catalyses the conversion of arginine to circulline and be used to

catalyses the conversion of arginine to circulline and patient, or

contraining a tumour and as melanoma, hepstoma or sarcoma in a patient, or

for treating and inhibiting metastases in a patient. When compared to

native arginine deiminase the compound retains most of its enzymatic

cativity, is far less antigenic, has a greatly extended circulating half-

life, and is much more efficacious in the treatment of tumours. The

sequence presented is the Qiardia intestinalis arginine deiminase gene,

catalyser. (Updated on 06-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                   Arginine deiminase; cytostatic; ADI; polyethylene glycol; PEG; arginine; citrulline; argininosuccinate synthase; argininosuccinate lyase; cancer; auxotrophic; tumour; melanoma; hepatoma; sarcoma; metastasis; antigenic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Compound for treating tumor such as melanoma, hepatoma or sarcoma in patient, comprises arginine deiminase covalently bonded by a linking group such as succinimide to polyethylene glycol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 43; DB 5; Length 580;
Pred. No. 55;
2; Mismatches 4; Indels

    Q. intestinalis arginine deiminase gene, QIAADIINT.

                                                                                                           ABG32001 standard; protein; 580 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (PHOE-) PHOENIX PHARMACOLOGICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 12; 59pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58.1%;
                                                                                                                                                                                                                                                                                                                                                                                                             19-SEP-2001; 2001WO-US029184.
                                                                                                                                                                                                                                                                                                                                                                                                                                           28-NOV-2000; 2000US-00723546
                              98 NNVLIPLEQOPTT 110
                                                                                                                                                                        (revised)
(first entry)
   14
   NNVLIQTDQOATT
                                                                                                                                                                                                                                                                                                                   Giardia intestinalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-619003/66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 580 AA;
                                                                                                                                                                                                                                                                                                                                                WO200244360-A2
                                                                                                                                                                        06-AUG-2003
15-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                               06-JUN-2002
                                                                                                                                          ABG32001;
   N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clark MA;
                                                                               RESULT 10
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The invention relates to inhibiting the replication of one or more viruses in an individual and involves administering to the individual accomposition comprising an arginine deaminase bonded to polyethylene glycol. The method is useful for inhibiting replication of one or more viruses e.g. hepatitis virus (hepatitis cirus-lb), in an individual, where the arginine deaminase is derived from Mycoplasma e.g. M. arginini, M. hominis, M. arthritidis and its combination. It is useful for treating an individual who is suspected of having been exposed to one or more viruses; for modulating nitric oxide levels in an individual. The method is also useful for treating a tumour and inhibiting replication of one ore hepatoma. The tumour is melanoma, sarcoma, or hepatoma. The tumour is hepatocellular carcinoma. The method is also useful for improving liver function in an individual. The present useful for improving liver function in an individual. The present
                                                 Inhibiting replication of viruses in individual, involves administering composition comprising arginine deiminase bonded to polyethylene glycol, to individual.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dog IgE epitope recognised by monoclonal antibody 5.91, SEQ ID 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8; Length 580;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 43; DB 8
Pred. No. 55;
2; Mismatches
                                                                                                                                                                              Claim 18; SEQ ID NO 17; 89pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADR10601 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ||:: ||| |||
168 NNMVFMRDQQITTR 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 NNVLIQTDQQATTR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-OCT-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
WPI; 2004-431965/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 580 AA;
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Gaps ö

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168

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8; Conservative

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(CAOY/) CAO Y.
 21-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            255
                                                                  Wang CY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADN24060;
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                   Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADN24060
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      ð
                                                                                                                                                                                                                                                                                   The present invention relates to a novel monoclonal antibody (I) that specifically binds to a mammalian IgE epitope, where the epitope is between aminon acids 145-166 or 356-374 of mammalian IgE, e.g. dog IgE. (I) is useful for testing an allergen reactivity of an IgE sample. The allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut and corn allergens. The sample is a biological sample collected from a consolidation or anaphylactic shock. The 5.91 and 3.76 monoclonal creating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal creating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal creating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal creating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal canine IgE epsilon-chain. Recognition of epsilon-chains from IgE from cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and 3.76 was examined. Both 5.91 and 6.76 IgE from cat and horse, but did not exhibit cross-reactivity with the epsilon-chain of IgE. either pig or human epsilon-chains of IgE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                   Novel antibody that specifically binds to mammalian IgE epitope, useful for testing an allergen reactivity of IgE sample, detecting mammalian IgE or treating asthma or anaphylactic shock.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen; immunoglobulin Einitatory; carrier protein; helper T cell epitope; antibody; allergy; allergic disease; immunisation; anti-allergic; anti-aschmatic; aschma; anaphylaxis; dermatitis.
Antiasthmatic; Antiallergic; Immunosuppressive; IgE; dog; asthma; anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 41; DB 8; Length 15; Pred. No. 2.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jog immunoglobulin E epsilon heavy chain SEQ ID NO:2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY79995 standard; protein; 312 AA
                                                                                                                                               (UYNC-) UNIV NORTH CAROLINA STATE
                                                                                                                                                                                                                                                                  Example 6; Page 9; 14pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1;
                                                                                                  15-JAN-2004; 2004WO-US003566.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55.4%;
                                                                                                                         16-JAN-2003; 2003US-0440472P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 RNNVLIQTDQQATT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RNDSPIQTDQYTTT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-593545/57.
                                  Canis familiaris.
                                                       402004065936-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 15 AA;
                                                                                                                                                                        Hammerberg B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W09967293-A1
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antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and anti-asthmatic properties. (I) induces polyclonal antibodies specific canti-asthmatic properties. (I) induces polyclonal antibodies specific for a target effector site on the epsilon-heavy chain of 198, and so preventing triggering and activation of mast cells and basophils and downregulation of 198 synthesis. Conjugates, or fusion peptides, containing (I) are used for active immunisation against 198-mediated allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy dermatitis. Nucleic acids that encode these compounds are useful for recombinant production of corresponding peptides or in DNA vaccines. CC conjugates of (I) that include a promiscuous T helper cell epitope. (functional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and maximize cross-reactivity to the natural target. They induce safe (non-anaphylactogenic) antibodies. AAYY9994 to AAY80084 represent amino acid sequences used in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                          New antigenic peptide from the CH3 domain of immunoglobulin E, fusions for immunization against allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              present invention describes immunoglobulin E (IgE)-CH3 domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55.4%; Score 41; DB 3; 64.3%; Pred. No. 63; iive 1; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Page 66-68; 155pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADN24060 standard; protein; 312 AA.
                                                                                                                                                  (UNBI-) UNITED BIOMEDICAL INC
                                                                     98US-00100287.
99WO-US013959.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-FEB-2002; 2002US-0360039P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacterial polypeptide #6713.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 RNNVLIQTDQQATT
                                                                                                                                                                                                                        Walfield AM;
                                                                                                                                                                                                                                                                                                 WPI; 2000-160578/14.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 312 AA;
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                                                                         20-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-DEC-2004
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                                                                                                                                                                                                                                                                                                                    baving an improved property comprises transforming a plant with the recombinant DNA construct and growing the transformed plant with the recombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant properties.

The recombinant DNA construct is useful for improving plant properties.

The recombinant DNA construct is useful for producing plants with improved plant properties, e.g. improved cold, heat or drought tolerance, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of photosynthesis or by prophyrus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition, improved lignin production or improved galactomannan condition, improved lignin production or improved galactomannan scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at sequence.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                               New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
                                                                                                                                                                                                                     The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polymucleotide encoding a polymeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IgE; immunoglobulin; antibody; heavy chain constant region; allergy; hypersensitivity; therapy; dog; antisense; immunomodulation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 41; DB 8; Length 312;
Pred. No. 63;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Canine IgE heavy chain constant region (exon 1-4 product).
                                                                         Goldman BS;
                                                                         Chen X,
                                                                                                                                                                                           Claim 1; SEQ ID NO 6713; 122pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note= "encoded by ACC"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW23067 standard; protein; 417 AA.
                                                                         Hinkle GJ, Slater SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :||||| |:: | |
159 DNVLIQKDEENTAR 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 NNVLIQTDQOATTR 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity 57.1.
Best Local 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (revised)
(revised)
                                                                                                   WPI; 2004-061375/06.
                              CHEN X.
GOLDMAN B S.
 HINKLE G J. SLATER S C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Canis familiaris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 312 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-JUN-2005
16-JUN-2005
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                              (CHEN/)
(GOLD/)
   HINK/)
                                                                        Cao Y,
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Isolated canine IgE heavy chain constant region DNA - useful to develop products for treatment of canine allergies and for immunomodulation in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This polypeptide is encoded by exons 1-4 (see AAT79278) of canine IgE heavy chain constant region (epsilon) genomic DNA. Another polypeptide, comprising the exon 5 and 6 product, is given in AAW23068. Recombinant peptides encoded by exons 1-6 can be produced in eukaryotic or prokaryotic cells. Such peptides, and antibodies raised against them, a used in methods to treat the manifestation of allergy in dogs, e.g. to treat Type I immediate hypersensitivity, and for immunomodulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Revised record issued on 30-JUN-2005 : Typo in comments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55.4%; Score 41; DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 88;
1; Mismatches
                                                                                                                                                                                                                                                               /note= "encoded by TCC"
204
                                                                                                                                                                                                                                                                                                                                        /note= "encoded by GAC"
                           note= "encoded by GCC"
                                                                         'note= "encoded by NNT"
                                                                                                                                                                                                                                 'note= "encoded by TGN"
                                                                                                                                                                             /note= "encoded by NNG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: August 30, 2006, 04:22:06 Job time : 55.5455 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure, Page 35-39; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Siefring AE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97WO-US002322.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RNNVLIQTDQQATT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 64.3
Matches 9; Conservative
                                                                                                                                  /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mermer B, Harris RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (IDEX-) IDEXX LAB INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1997-425031/39.
                                                                                                                                                       Misc-difference 175
                                                                                                                                                                                                        Misc-difference 176
                                                                                                       Misc-difference 174
                                                                                                                                                                                                                                                            Misc-difference 203
Misc-difference 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAT79278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 417 AA;
                                                   Misc-difference
                                                                                                                                                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                           WO9730156-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                               21-AUG-1997
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protein search, using sw model OM protein -

Run on:

(without alignments) 161.448 Million cell updates/sec August 30, 2006, 04:29:42; Search time 8.93939 Seconds

US-10-758-165A-3

1 RNNVLIQTDQQATTR 15 score: Sequence: Perfect

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

of hits satisfying chosen parameters: Total number

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq Post-processing: Minimum Match 08 Maximum Match 1008

Listing first 45 summaries

Database

1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:* PIR_80:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RIES	Description			ardinine deiminase	hypothetical prote	protein H42K12.1 [glutamate synthase	hypothetical prote	probable receptor-	probable membrane	hypothetical prote	sucrose alpha-gluc	probable translati	hypothetical prote			o	protein F39E9.5 [i	serine proteinase	hypothetical prote	GTP-binding protei	histidine protein	probable sensor hi	protein-tyrosine-p	targeted effector	virulence protein	glutamate receptor	kainate-binding pr	111111111111111111111111111111111111111	rangiarion initia
SUMMARIES		F95884	H84219	T45064	T32446	A89460	S61041	E85042	H84421	G97191	AI2531	A23945	H64842	H90785	F85645	S67804	872252	B88095	AG2150	T24441	C70163	G98126	B95261	A53889	T43622	501054	S07062	151201	C81060	
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	Query Match Length	917	285	580	312	312	2145	263	716	138	829	1827	128	128	128	1017	140	202	407	412	433	441	441	468	468	468	487	487	962	
عِن	Query Match	60.8	58.8	58.1	55.4	55.4	വ	52.7	52.7	51.4	51.4	51.4	50.0	50.0	50.0	49.3	48.6	48.6	48.6	48.6	48.6	48.6	48.6	48.6	48.6	48.6	48.6	٠	48.6	
	Score	45	43.5	43	41	41	41	39	39	38	38	38	37	37	37	36.5	36	36	36	36	36	36	36	36	36	36	36		36	
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AD1728 T15232	T20181 JC5144 T20180	T20179 AD2267	T14523 AC0587	B90719 C85569	E64804 T20321	B84597	S73498	T09019
0 0	200	7 7	0 0	7 7	0 0	7	8	7
1157	1449 1464 1584	1586	185 225	225	225	276	345	386
8 4 8 6 6 6	4 4 8 4 6 8 6 6 9 6 9 6	48.6 48.6	47.3	47.3	47.3	47.3	47.3	47.3
386	3 9 9	36 36	32 32	35 35	35 35	35	32	35
30 31	3 8 8 4 3 8	3 9 3 9 8	37 38	3 4 0	41 42	43	44	45

ALIGNMENTS

RESULT	F95884

probable sensory histidine kinase protein [imported] - Sinorhizobium meliloti (strain 10 C;Species: Sinorhizobium meliloti (c)Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004 C;Accession: F95884

R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan R;Finan, T.M.; Call Sci. 18, 9889-9894, 2001 A;Title: The complete sequence of the 1.683-Kb pSymB megaplasmid from the N2-fixing endo A;Reference number: A95842; MUID:21396508; PMID:11481431

A, Accession: F95884

A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1917 < KUR>
A/Grose-references: UNIPROT:022WJ7; UNIPARC:UPI00000CB4C5; GB:AL591985; PIDN:CAC48742.1;
A/Experimental source: strain 1021, megaplasmid pSymB
A/Status. F; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, Br;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, Dela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A,Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner S.; Wells, D.H.; Wong, K.; Yeh, K.
A,Fittle: The composite genome of the legume symbiont Sinorhizobium meliloti.
A,Reference number: A96039; WUID:21368234; PMID:11474104

C;Genetics: A;Gene: SMb20356

A; Genome: plasmid

Gaps . 0 Length 917; 2; Indels DB 2; ed. No. 3.6; Mismatches Score 45; Pred. No. 4 ; 60.8%; ilarity 57.1%; Conservative Query Match Best Local Similarity Matches 8; Conserv

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hypotherical protein Vng0617h [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
R;Ng; W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablo Jung, K.H.; Alam, M.; Freitas, T. 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li A;Reference number: A84160; MUID:20504483; PMID:11016950

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A,Title: Genome sequence of the nematode C. elegans: a platform for investigating biology A,Reference number: A75000, MUID:99069613; PMID:9851916
A,Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_elegans/ A,Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 15312 <STO>
A;Cross-references: UNIPARC:UPI000017A469; GB:chr_X; PIDN:AAB71265.1; PID:g2435556; GSPDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                glutamate synthase (NADH2) (EC 1.4.1.14) glt1 precursor [similarity] - yeast (SaccharomytAlternate names: protein D148; protein YDL171c C;Species: Saccharomyces cerevisiae C;Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 12-Jul-2004 C;Accession: S61041; S67723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 1-2145 <POH>
A;Cross-references: UNIPARC:UP100001682D6; EMBL:267750; NID:g1061256; PIDN:CAA91574.1; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-2145 <POW>
A;Cross-references: UNIPARC:UP100001682D6; EMBL:Z74219; NID:g1431273; PIDN:CAA98745.1; P
                                                                                                                                                                                        C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 31-Dec-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Superfamily: glutamate synthase (NADH/NADPH), eukaryotic type
C;Keywords: 3Fe-4S; metalloprotein; oxidoreductase; transmembrane protein
F;1-53/Domain: propeptide #status predicted <PRO-
F;54-2145/Product: glutamate synthase #status predicted <MAT>
F;1077-1093/Domain: transmembrane #status predicted <TM1>
F;1172-1188/Domain: transmembrane #status predicted <TM2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;54/Active site: Cys #status predicted
F;1185,1191,1196/Binding site: 3Fe-4S cluster (Cys) (covalent) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  submitted to the Protein Sequence Database, July 1996 A, Reference number: S67708
                                                                                                                                      protein H42K12.1 [imported] - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 55.4%; Score 41; DB 2; Best Local Similarity 57.1%; Pred. No. 55; Matches 8; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                        C,Accession: A89460
R,anonymous, The C. elegans Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Reference number: S61010
A;Reference number: S61010
A;Accession: S61041
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3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 41;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A, Experimental source: strain S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Note: Similar to protein kinase
                                                                                                                                                                   C;Species: Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55.4%;
57.1%;
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159 DNVLIQKDEENTAR 172
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                                                                                                                                                                                                                                                                             Science 282, 2012-2018, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
A;Molecule type: DNA
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A;Title: Cloning and expression of a prokaryotic enzyme, arginine deiminase, from a prim A;Reference number: 222902; MUID:98136144; PMID:9468500
A;Accession: T45064
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-580 < KNO>
A;Residues: 1-580 < KNO>
A;Cross references: UNIPROT:027657; UNIPARC:UPI000004CCBB; EMBL:U49236; PIDN:AAC06116.1
C;Wunction: BC 3.5.3.6 [validated, MUID:98136144]
C;Superfamily: Giardia intestinalis arginine deiminase
C;Keywords: hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein H42K12.1 - Caenorhabditis elegans (fragment)

Listate caenorhabditis elegans
CjBecites Caenorhabditis elegans
CjBecites 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 05-Oct-2004
CjAccession: T32446
Ki,Maggi, L.; Harper, M.
Submitted the EMBL Data Library, September 1997
A.Description: The sequence of C. elegans cosmid H42K12.
A.Reference number: Z21169
A.Accession: T32446
A.Accession: T32446
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Residues: 1-312 <AMG>
A.Residues: 1-312 <AMG>
A.Residues: 1-312 <AMG>
A.Residues: Labrates: UNIPARC:UPI000017A469; EMBL:ARF026207; PIDN:AAB71265.1; GSPDB:GN00028
A.Experimental source: strain Bristol N2; clone H42K12
C.Genetics:
                             A;Molecule type: DNA
A;Residues: 1-285 <STO>
A;Crostarences: UNIPROT:Q9HRN4; UNIPARC:UPI0000636A7; GB:AE004437; NID:g10580210;
C;Genetics:
A;Gene: VNG0617H
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C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
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                                                                                                                                                                                              Length 285;
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Pred. No. 5.2;
); Mismatches 4; Indels
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A;Introns: 4/2; 40/3; 106/1; 167/1; 196/2; 251/3
                                                                                                                                                                                                58.8%; Score 43.5; Di
58.8%; Pred. No. 1.8;
ive 2; Mismatches
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|NNVLLQTDSETELTTTR 228
                                                                                                                                                                                                                                                                                                                2 NNVLIQTDQQ---ATTR 15
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Similarity 57.1%;
8; Conservative ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 NNVLIQTDQQATTR 15
                                                                                                                                                                                              Query Match 58.8
Best Local Similarity 58.8
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 8; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 8; Conserv
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     A,Status: preliminary
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R; Knodler, L.A.; Sek
J. Biol. Chem. 273,
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Gaps

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A;Reference number: A96900; MUID:21359325; PMID:21359325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Accession: AI2531
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 9, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana;
A;Reference number: AB1807; MUID:21595285; PMID:11759840
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A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Rodlecule type: 1-829 «KUR»
A;Rodlecule type: 1-829 «KUR»
A;Rodlecule type: 1-829 «KUR»
A;Experimental source: strain PCC 7120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     aypothetical protein alr7540 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120be
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FBSS Lett. 148, 321-325, 1982
A;Title: N-terminal sequences of pig intestinal sucrase-isomaltase and pro-sucrase-isoma
A;Reference number: A25987; MUID:83105704; PMID:7152027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 138;
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A;Residues: 2-32,'XXX',36-38;1008,'N',1010-1014,'E' <SJ2>
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69;
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Pred. No. 9;
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A;Residues: 1-1827 <HUN>
A;Cross-references: UNIPARC:UPI00001729E8
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Best Local Similarity 53.8
Matches 7; Conservative
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Best Local Similarity
7; Conserve
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A,Molecule type: DNA
A,Residues: 1-138 <KUR>
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A;Genome: plasmid
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                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein AT4g03350 [imported] - Arabidopsis thaliana (c.Species: Arabidopsis thaliana (mouse-ear cress) (c.Species: Arabidopsis thaliana (mouse-ear cress) (c.Species: Arabidopsis thaliana (mouse-ear cress) (c.Space: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004; C.Saccession: B85042 (S.Species) 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable receptor-like protein kinase [imported] - Arabidopsis thaliana (Grobable receptor-like protein kinase [imported] - Arabidopsis thaliana (Mouse-ear cress)

C;Species: Arabidopsis thaliana (Mouse-ear cress)

C;Date: O2-Eeb-2001 #sequence_revision 02-Feb-2001 #text_change 31-Dec-2004

C;Accession: H84421

R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Reference number: A84420; MUID:20083487; PMID:10617197
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C;Species Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: G97191
S;Nolling, J: Breton, G:, Omelotenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J. Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana. A;Reference number: A85001; MUID:20083488; PMID:10617198
A;Accession: E85042
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-263 <STO>
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Pred. No. 12;
4; Mismatches 3; Indels
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Best Local Similarity 53.3%; Pred. No. 38;
Matches 8; Conservative 3; Mismatches
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C,Superfamily: Receptor-like protein kinase
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QSNRIIQTDQQPQER 582
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1145 RRNVVVQTDGQLRT 1158
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RTNQVVQTTEQAST. 158
                                                                                      RNNVLIQTDQQATT 14
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Best Local Similarity 50.v-
T; Conservative
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A;Residues: 1-716 <STO>
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A;Gene: AT4g03350
A;Map position: 4
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K.; Han, C.G. H.

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A;Status: pre-infinary
A;Molecule type: DNA
A;Mosiduse: 1-128 «STO»
A;Cross-references: UNIPROT:08XAU5; UNIPARC:UPI00000D067E; GB:AE005174; NID:g12514367; P
A;Experimental source: strain O157:H7, substrain EDL933
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A;Residues: 1-1017 <ALT>
A;Cross-references: UNIPROT:P35688; UNIPARC:UP1000012E93A; EMBL:Z74288; NID:g1431407; PI
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R;Mucller, A.; Xu, G.; Wells, R.; Hollenberg, C.P.; Piepersberg, W.
submitted to the EMBL Data Library, March 1994
A;Description: LRGI is expressed during sporulation in Saccharomyces cerevisiae and cont
                                                                                                                                                                                                                                                                                                                                                                                  A,Cross-references: UNIPROT:08XAUS; UNIPARC:UPI0000D067E; GB:BA000007; PIDN:BAB34679.1;
A,Experimental source: strain 0157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ypothetical protein 21509 [imported] - Escherichia coli (strain 0157:H7, substrain EDL9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Accession: F95645
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew RiPerna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew Iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
                R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and A;Reference number: A99629; MUID:21156231; PMID:11288796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INGI protein - yeast (Saccharomyces cerevisiae)
NyAlternate names: protein D0764; protein YDL240w
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Accession: S67804; S43158; S47956
R;Alt-Moerbe, J.; Schneider, C.; Moro, M.
submitted to the Protein Sequence Database, July 1996
A;Reference number: S67798
A;Reference number: S67798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Dec-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50.0%; Score 37; DB 2; Length 128; 57.1%; Pred. No. 13; tive 1; Mismatches 5; Indels
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C,Superfamily: translation initiation inhibitor, TdcF type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Gene: ECs1256
C,Superfamily: translation initiation inhibitor, TdcF type
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8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
nes 8; Conserv
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                                                                                                                                                                                                                                                                            A, Status: preliminary A, Molecule type: DNA
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Best Local
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Matches
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                                                                                                                                                                                  A/Rocession: A29163
A/Rocession: UNIPARC: UPT00001729EB
C/COmment: Carbohydrate analysis of the mature enzyme complex indicates both N- and O-li
C/COmplex: the two product chains remain associated after cleavage
C/Function: A180-
A/Boscription: oligo-1,6-glucosidase catalyzes the hydrolysis of 1,6-alpha-D-glu
A/Pathway: carbohydrate digestion
C/Function: sucrose alpha-glucosidase catalyzes the hydrolysis of the 1,2-alpha-D-glu
A/Pathway: carbohydrate digestion
C/Superfamily: sucrase/isomaltase; sucrase/isomaltase homology; trefoil homology
C/Roywords: carbohydrate digestion; duplication; glycoprotein; glycosidase; hydrolase; m
F/2-1007/Product: oligo-1,6-glucosidase (isomaltase chain) #status experimental <1SO-
F/13-32/Domain: membrane associated #status predicted <TWM>
F/13-32/Domain: serine/threonine-rich
C/ALOFA CANONINE-ROOFA CANONINE-ROOFA
C/ALOFA CANONINE-ROOFA
C/ALOFA
C/AL
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C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 31-bec-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;63-109/Domain: trefoil homology <TRPI>
F;189-840/Domain: sucrase/isomaltase homology <SIM>
F;180-840/Domain: trefoil homology <TRF2
F;1008-1827/Domain: trefoil homology <TRAIS
F;1008-1827/Product: sucrose alpha-glucosidase (sucrase chain) #status experimental <SUC
F;1062-1734/Domain: sucrase/isomaltase homology <SIM>
F;12/Binding site: carbohydrate (Thr) (covalent) #status experimental
F;99,455,859,896,904,1235,1303,1325,1340,1364,1368,4403,1535,1572,1748,1763,1799/Binding
F;1007-1008/Cleavage site: Arg-Ile (trypsin) #status predicted
A;Cross-references: UNIPARC:UPI00001729E9; UNIPARC:UPI00001729EA
R;Frank, G.; Brunner, J.; Jauser, H.; Wacker, H.; Semenza, G.; Zuber, H.
ESES Lett. 96, 183-188, 1978
A;Title: The hydrophobic anchor of small-intestinal sucrase-isomaltase. N-terminal seque
A;Reference number: A29163; MUID:79086207; PMID:729784
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Pred. No. 1.7e+02;
2; Mismatches 5; Indels
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Best Local Similarity 50.0%;
Matches 7; Conservative 5
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Gaps

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A; Molecule type: DNA
A; Residues: 1-530, 'Q', 532-765,'S', 767-790, 'T', 792-820, 'Q', 822-837,'S', 839-848,'L', 850-89
A; Creatences: UNIPARC; UPIO000168CBB; EMBL: X78453; NID: 9468734; PID: 9468735
R; Mueller, L., Xu, G.; Wells, R.; Hollenberg, C.P.; Piepersberg, W.
Nucleic Acids Res. 22, 3151-3154, 1994
A; Title: LRG1 is expressed during sporulation in Saccharomyces cerevisiae and contains m
A; Reference number: S47956; MUID: 94344779; PMID: 8065929
                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: DNA
A;Residues: 28-89;98-136,'MF',139-148;157-184;419-474;755-765,'S',767-790,'T',792-820,'(
A;Cross-references: UNIPARC:UP1000017B2C8; UNIPARC:UP1000017B2C9; UNIPARC:UP1000017B2CA,
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E;28-89/Domain: LIM metal-binding repeat homology <LIMI>
E;28-484/Domain: LIM metal-binding repeat homology <LIM2>
E;157-184/Domain: LIM metal-binding repeat homology #status atypical <LIM3>
E;157-184/Domain: LIM metal-binding repeat homology y status
E;348-364/Domain: transmembrane #status predicted <TM1>
E;419-474/Domain: LIM metal-binding repeat homology <LIM4>
E;487-503/Domain: transmembrane #status predicted <TM2>
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49.3%; Score 36.5; DB 2; Length 1017;
Best Local Similarity 50.0%; Pred. No. 1.7e+02;
Matches 9; Conservative 3; Mismatches 1; Indels 5
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A;Gene: SGD:LRG1
A;Cross-references: SGD:S0002399; MIPS:YDL240w
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583 NLVIQTDDPSSSQQVSTR 600
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A;Reference number: S43158
A;Accession: S43158
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Q35k12 Q487c7 Q5v1k0 Q9c2a6 Q9c2a6 Q6jpv5 Q6jpv7 Q84i43 Q54j46 Q65am3 Q2skc0 Q97gk0

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NUCLEOTIDE SEQUENCE.
NUCLEOTIDE SEQUENCE.
NUCLEOTINE=20363099; PubMed=10907853; DOI=10.1093/dnares/7.3.217;
Kaneko T., Katch T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
"Structural analysis of Arabidopsis thaliana chromosome 3. II.
Sequence features of the 4,251,695 bp regions covered by 90 P1, TAC
and BAC clones.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-007-2000, sequence version 1.
07-FEB-2006, entry version 17.
07-FEB-2006, entry version 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S., Submitted (MAY-2000) to the {\tt EMBL/GenBank/DDBJ} databases.
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2081 AA; 232853 MW; D3603E1F85EFFF29 CRC64;
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092WJ7 RHIME
092WJ7 RHIME PRELIMINARY; FRT; 917 AA.
AC 092WJ7.
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 07-FEB-2006, entry version 20.
DF 07-FEB-2006, entry version 20.
DF William Finase protein.
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53.3%; Pred. No. 33;
iive 4; Mismatches
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                                                         NPVSF
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Q487C7_C
Q5VLK0_N
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06JPV5 P
06JPV7 P
084143 P
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Q2SKC0
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TARR; AX328470; -.
InterPro; IPR009605; DUF1216.
Pfam; PP06746; DUF1216; 2.
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1302 KNEILMQADSQATTQ 1316
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NUCLEOTIDE SEQUENCE.
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о9гн98;
  SEQUENCE
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lactobacill
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                                                                                                                              August 30, 2006, 04:22:32 ; Search time 58.4848 Seconds (without alignments) 237.245 Million cell updates/sec
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ambystoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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O5c6i4
O5wv87
O5x3u5
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07r036
07r036
07zxi57
02xi57
08h475
06fp28
04svf5
07xuq6
03m1k9
06cmk0
012680
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Q6ma42
Q74k19
Q9zgz6
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055b16
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Q5qvd0
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                 GenCore version 5.1.9 (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                              2849598
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                                                                                                                                                                                                                                                                                                                                                                   2849598 segs, 925015592 residues
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O27657_GIALA
O7ZX14_XENLA
Q8H475_ORYSA
Q6FP28_CANGA
Q4SVF5_TETNG
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QETLS3 CANGA
Q75917 ASHGO
Q6D5C2 ERWCT
Q37FN1 RHOPA
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Q7XUQ6_ORYSA
Q3M1K9_ANAVT
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QSWV87 LEGPL
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Q9XRP4_AMBME
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Q9ZQZ6_ARATH
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Maximum Match 100%
Listing first 45 summaries
                                                                                                protein search, using sw model
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1: uniprot_sprot:*
2: uniprot_trembl:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                   length: 0
length: 2000000000
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74 /
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Match Length DB
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Database

Perfect score:

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Gaps

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STRAIN-EAX4,

SUGARDA B.

SURGARDA B.

B. PubMed=15875012, DOI=10.1038/nature03481;

PubMed=15875012, DOI=10.1038/nature03481;

B. Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.A.,

B. Sucgard R., Bacrhaman M., Song J., Oleen R., Szafranski K., Xu Q.,

R. Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,

Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,

Pilcher K., Chen G., Saunders D., Sodergren E.J., Davis P.,

Rerbornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,

Farbrother P., Desany B., Just E., Morio T., Rost R., Goodhead I.,

Rooper J., Haydock S., Van Driessche N., Cronin A., Goodhead I.,

A muzny D.M., Mourier T., Pain A., Lu M., Harper D., Lindsay R.,

A Hauser H., James K.D., Quiles M., Madan Babu M., Saito T.,

Buchrieser C., Wardroper A., Felder M., Thangavelu M., Johnson D.,

Knightes A., Loulseaded H., Mungall K.L., Oliver K., Price C.,

Quail M.A., Urushihara H., Hernandez J., Simmonds M.N., Spiegler S.,

A sanders M., Ma J., Kohara Y., Sharp S., Simmonds M.N., Spiegler S.,

Tivey A., Sugano S., White B., Walker D., Woodward J.R., Minckler T.,

Tanaka Y., Shaulsky G., Schleicher M., Weinstock G.M., Rosenthal A.,

Kay R.R., Williams J.G., Dear P.H., Noegel A.A., Barrell B.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bichinger L. Pachebat J.A. (Glockner G., Rajandream M.A., Bichinger L., Pachebat J.A. (Glockner G., Rajandream M.A., Buchinger B., Pachebat J.A. (Glockner G., Szafranski K., Xu O., Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F., Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudder P., Fey P., Prilcher K., Chen G., Saunders D., Sodergren E.J., Davis P., Perhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N., Farbrother P., Desany B., Just E., Morio T., Rost R., Churcher C.M., Parbother P., Desany B., Just E., Morio T., Goodhead I., Muzny D.M., Mourier T., Pain A., Lu M., Harper D., Lindsay R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 435:43-57(2005).
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The genome of the social amoeba Dictyostelium discoideum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AAF101000301; EAL60430.1; -; Genomic_DNA.
Hypotherical protein.
SEQUENCE 649 AA; 77580 MW; B366A94429ECDD53 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein.
ORFNames=DDB0216848;
Dictyostellum discoideum (Slime mold).
Bukaryota, Mycetczoa, Dictyostellida, Dictyostellum.
NCBI_TaxID=44689;
Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.
NCBI_TaxID=44689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59.5%; Score 44; DB 2;
llarity 61.5%; Pred. No. 32;
Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-MAY-2005, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 649 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        611 MNIIIQTQQQKPT 623
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                                                                                                                                                                                        NUCLEOTIDE SEOUENCE
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tes 8; Conserv
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Q55B16;
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Hash; passay incomparation; pre-project process.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0003677; F:DNA binding; IEA.

GO; GO:00016301; F:Kinase activity; IEA.

GO; GO:00016301; F:Kinase activity; IEA.

GO; GO:000156; F:two-component response regulator activity; IEA.

GO; GO:000155; F:two-component sensor molecule activity; IEA.

GO; GO:000155; F:two-component signal transduction; IEA.

GO; GO:000160; P:two-component signal transduction system (p. . .; IEA.)

GO; GO:000160; P:two-component signal transduction system (p. . .; IEA.)

GO; GO:000160; P:two-component signal transduction system (p. . .; IEA.)

InterPro; IPR003564; ATP DA ATPASE.

InterPro; IPR003561; His kin like C.

InterPro; IPR001561; His kin like C.

InterPro; IPR001561; His kin like C.

InterPro; IPR001561; His kin like C.

InterPro; IPR00175; Response reg.

Ffam; PF00512; HaMP; 1.

Ffam; PF00512; HaMP; 1.

BR Ffam; PF00512; HaMP; 1.

Ffam; PF00175; Response reg; 3.

PFam; PR000175; Response reg; 2.

PRINTS; PR00174; HAMP; 1.

PRINTS; PR00174; HAMP; 1.

PRADET: SHAMP; 1.

PRADET: SHA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                        Finan T.M., Weidner S., Wong K., Buhrmester J., Chain P., Vorhoelter F.J., Hernandez-Lucas I., Becker A., Cowie A., Gouzy J., Golding B., Puehler A., "The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21396508; PubMed=11481431; DOI=10.1073/pnas.161294698;
                                                                                                                                      Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 45; DB 2; Length 917; Pred. No. 31;
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PROSITE; PS50109; HIS KIN; 1.
PROSITE; PS50110; RESPONSE_REGULATORY; 2.
COMPLETE PSTOTE PSTOTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fixing endosymbiont Sinorhizobium meliloti.";
Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ©54AY3_DICDI PRELIMINARY; PRT; 649 AA. 054AY3; 24-MAY-2005, integrated into UniProtKB/TrEMBL. 24-MAY-2005, sequence version 1. 07-FEB-206, entry version 3. Hypothetical protein. RFNames=DB0215056;
                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                             OrderedLocusNames=RB0342; ORFNames=SMb20356; Rhizobium meliloti (Sinorhizobium meliloti).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AL591985; CAC48742.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00304; HAMP; 1. SMART; SM00387; HATPARG, 2. 1. SMART; SM00388; HISKA; 1. SMART; SM00448; REC; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57.1%;
                                                                                                                                                                                        Rhizobiaceae; Sinorhizobium.
NCBI_TaxID=382;
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188 RNEVVVQTEKTATT 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; F95884; F95884.
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Best Local Similarity
Matches 8; Conserva
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à 요 054AY3 1D 05 AC 05 DT 24 DT 24 DT 07 DB HY GN OR

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Gaps

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Length 649; 3; Indels

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2 NNVLIQTDQQ---ATTR 15
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                                                                                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein.
OrderedLocusNames=lpl1930;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 57.1
nes 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |||:|| ||: ||
NNVIIQKDQKGPSR
                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=6182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OSWV87:
                                                                                                                                                                Q5C614_SCHJA
Q5C614;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                       Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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WEDLINB=20504483; PubMed=11016950; DOI=10.1073/pnas.190337797;

MW V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
Alam W., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., Dassarma S.;
Hauser H., James K.D., Quiles M., Madan Babu M., Saito T.,
Buchrieser C., Wardroper A., Felder M., Thangavelu M., Johnson D.,
Knights A., Loulseged H., Mungall K.L., Oliver K., Price C.,
Quail M.A., Urushihara H., Hernandez J., Rabbinowitsch E., Steffen D.,
Sanders M., Ma J., Kohara Y., Sharp S., Simmonds M.N., Spiegler S.,
Tivey A., Sugano S., White B., Walker D., Woodward J.R., Winckler T.,
Tanaka Y., Shaulsky G., Schleicher M., Weinstock G.M., Rosenthal A.,
Cox E.C., Chisholm R.L., Gibbs R.A., Loomis W.F., Platzer M.,
KAY R.R., Williams J.G., Dear P.H., Noegel A.A., Barrell B.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                              CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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                                                                                                                                                                                                                                 "The genome of the social amoeba Dictyostelium discoideum."; Nature 435:43-57(2005).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58.8%; Score 43.5; DB 2; Length 285; 58.8%; Pred. No. 15; ive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59.5%; Score 44; DB 2; Length 649; 61.5%; Pred. No. 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    l protein.
649 Aa; 77580 MW; B366AD152ACDDA23 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Archaea; Buryarchaeota; Halobacteria; Halobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       285 AA; 29163 MW; 31223D1A949BC1B3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Halobacterium salinarium (Halobacterium halobium)
                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AAFI01000013; EAL71869.1; -; Genomic DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
STRAIN-NRC-1 / ATCC 700922 / JCM 11081;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9HRN4;
01-MAR-2001, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 285 AA.-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE005010; AAG19124.1; -; Genomic_DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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BioCyc; HSP64091:VNG0617H-MONOMER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Halobacteriaceae; Halobacterium.
NCBI TaxID=2242;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2001, sequence version 07-FEB-2006, entry version 14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9HRN4_HALSA PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OrderedLocusNames=VNG0617H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ||::||| || || || 611 NNIIIQTQQQKPT 623
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Matches 8; Conservative
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Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                              preliminary data.
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SEQUENCE 285 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical
SEQUENCE 64
                                                                                                                                                                                                                Kuspa A.;
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8 셤 RESULT CONTROL OF CONT

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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
Liu F., Lu J., Hu W., Wang S.-Y., Cui S.-J., Chi M., Yan Q.,
Liu F., Lu J., Hu W., Wang S.-Y., Cui S.-J., Shang X.-L., Wang X.-Y., Song H.-D., Xu X.-N., Wang J.-J., Zhang X.-L., Wang Z.-Q.,
Xue C.-L., Brindley P.J., McManus D.P., Yang P.-Y., Feng Z., Chen Z.,
Han Z.-G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
PubMed=15467720; DOI=10.1038/ng1447;
Cazalet C., Rusniok C., Brueggemann H., Zidane N., Magnier A., Ma L.,
Tichit M., Jarraud S., Bouchier C., Vandenesch F., Kunst F.,
Etienne J., Glaser P., Buchrieser C.;
Etienne J., Glaser P., Buchrieser C.;
"Evidence in the Legionella pneumophila genome for exploitation of host cell functions and high genome plasticity.";
                                                                                                                                                                                                                                                                                                                       Trematoda; Digenea; Strigeidida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Transcriptomic and Proteomic Analyses of the Human Blood Fluke,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Legionella pneumophila (strain Lens).
Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
Legionellaceae; Legionella.
NCBI_TaxID=297245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schistosoma japonicum.";
Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          161 AA; 18352 MW; 1A6BF6544526AE04 CRC64;
                                                                                                                                                                                                                    08-NOV-2005, sequence version 2.
07-FEB-2006, entry version 5.
SJCHGC07693 protein (Fragment).
Schistosoma japonicum (Blood fluke).
Bukaryota, Metazoa, Platyhelminthes; Trematoda, D. Schistosomatoidea, Schistosomatidae, Schistosoma.
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                                                                                                                                                                                            12-APR-2005, integrated into UniProtKB/TrEMBL
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                                                                                                                                                161 AA.
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3; Mismatches
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LegioList; lp11930; -.
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                                                                                                                                          PRT;
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212 NNVLLQTDSETELTTR 228
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Complete proteome, Hypothetical protein.

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preliminary data.
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                                                                                                                                                                                                                                       Complete proteome.
SECUENCE 463 AA;
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O7R036;
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Q27657;
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Q7R036 GIALA
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027657 GIP
027657 GIP
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DT 01-NC
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OS GIACO
OC BURAN
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(1)
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Chien M., Morozova I., Shi S., Sheng H., Chen J., Gomez S.M.,
Asamani G., Hill K., Nuara J., Peder M., Rinner J., Greenberg J.J.,
Steshenko V., Park S.H., Zhao B., Teplitskaya E., Edwards J.R.,
Pampou S., Georghiou A., Chou I.-C., Jannuccilli W., Ulz M.E.,
Kim D.H., Geringer-Sameth A., Goldsberry C., Morozov P., Fischer S.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
PubMed=11467720; DOI=10.1038/ng1447;
Cazalet C., Rueniok C., Brueggemann H., Zidane N., Magnier A., Ma I Tichit M., Jarraud S., Bouchier C., Vandenesch F., Kunst F., Etienne J., Glaser P., Buchrieser C., andenesch F., Kunst F., Etienne J., Glaser P., Buchrieser C., host cent in the Legionella pneumophila genome for exploitation of host cell functions and high genome plasticity.";
Nat. Genet. 36:1165-1173(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Legionella pneumophila subsp. pneumophila (strain Philadelphia 1 /
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23-NOV-2004, sequence version 1.
07-FBE-2006, entry version 8.
Hypothetical protein.
OrderedLocusNames=lpp1939;
Legionella protemophila (strain Paris).
Bacteria, Proteobacteria; Gammaprotecobacteria; Legionellales;
Legionellaceae; Legionella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
Legionellaceae; Legionella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58.1%; Score 43; DB 2; Length 417; 69.2%; Pred. No. 30; ive 1; Mismatches 3; Indels
                                            Query Match 58.1%; Score 43; DB 2; Length 416; Best Local Similarity 69.2%; Pred. No. 30; Matches 9; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; CR628336; CAH13091.1; -; Genomic_DNA.
LegioList; lppl339; -.
Complete proteome; Hypothetical protein.
SEQUENCE 417 AA; 49131 MW; 01F6BA54E430C7E2 CRC64;
416 AA; 48862 MW; 0E153EDD3778559E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
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                                                                                                                                                                                                                                                                                                               417 AA.
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                                                                                                                                                                                                                                                                                                            QSX3US_LEGPA PRELIMINARY; PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-NOV-2004, sequence version 1.
07-FEB-2006, entry version 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QSZUS1_LEGPH PRELIMINARY;
QSZUS1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EbhA protein.
OrderedLocusNames=lpg1957;
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                                                                                                                                                                          |||||| :|| ||
NNVLIPLEQOPTT 75
                                                                                                                                            2 NNVLIOTDOOATT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 NNVLIPLEQOPTT 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 69.2
les 9; Conservative
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       SEQUENCE
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QSZUS1_LE
                                                                                                                                                                                                                                                              RESULT 8
OSX305 LBD
OSX305 LBD
DT 23-N
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Cayanis E., De Jong P.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-WB C6;
Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Olsen G.J., Sogin M.L.;
Olsen G.J., Sogin M.L.;
"Draft sequence of the Giardia lamblia genome.";
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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  Segal G., Qu X., Rzhetsky A., Zhang P., Cayanis E., De Jong
Ju J., Kalachikov S., Shuman H.A., Russo J.J.;
"The genomic sequence of the accidental pathogen Legionella
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01-NOV-1996, entry version 20.
Arginine deiminase (EC 3.5.3.6).
Giardia lamblia (Giardia intestinalis).
Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
NCBL_TaxID=5741;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
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                                                                                                                                                                                                                                                                                                                                                 58.1%; Score 43; DB 2; Length 463; 69.2%; Pred. No. 34; ive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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InterPro; IPR003198; Amidino.trans.
Pfam; PF02274; Amidinotransf; 1.
SEQUENCE 505 AA; 55735 MW; 99E2CBF5B56824B0 CRC64;
                                                                                                                                                                                                                                                                                                 463 AA; 54449 MW; BE76CBED5D81D264 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 505 AA.
                                                                                                                                                                                                                             EMBL; AE017354; AAU28026.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 43; DB Pred. No. 38;
Zhang P., Cay
H.A., Russo J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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OF PEB-2006, entry version 12.
GLP 456 18539 20056.
Giardia-lamblia ATCC 50803.
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                                                                               pneumophila.";
Science 305:1966-1968(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93 NNMVFMRDQQITTR 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 NNVLIQTDOOATT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87 NNVLIPLEQQPTT 99
                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 69.2
Matches 9; Conservative
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Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oryza sativa (japonica cultivar-group).
Bukaryota, Vitidiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
Ehrhartoideae; Oryzeae; Oryza.
                       Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / Match 56.1%; Score 41.5; DB 2; Length 854; Local Similarity 78.6%; Pred. No. 1.4e+02; les 11; Conservative 0; Mismatches 2; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sasaki T., Matsumoto T., Yamamoto K.; "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7, PAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 106;
                                                                                                                                                                                                                                                                                                                                                       GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0017111; F:nucleoside-triphosphatase activity; IEA.
GO; GO:0000166; F:nucleotide binding; IEA.
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                                                                                                                                                  Klein S., Strausberg R., Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone:P0470D12.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATP-binding; Nuclectide-binding.
SEQUENCE 854 AA; 93597 MW; F91339E502C41BB3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AP004300; BAC15985.1; -; Genomic_DNA.
Gramene; Q8H475; -.
Hypothetical protein.
SEQUENCE 106 AA; 12281 MW; 8016731B1945298F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55.4%; Score 41; DB 2;
46.7%; Pred. No. 15;
tive 6; Mismatches 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          centr,
                                                                                                                                                                                                                                                                                                          EMBL; BC044980; AAH44980.1; -; mRNA.
HSSP; Q01853; 1R7R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-FEB-2006, entry version 8.
Hypothetical protein P0470D12.115.
                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR003593; AAA ATPase.
InterPro; IPR003959; AAA ATPase.
InterPro; IPR003960; AAA ATPase.
Pfam; PP00004; AAA; 2.
SMART; SM00382; AAA; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                               initiative.";
Dev. Dyn. 225:384-391(2002).
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Best Local Similarity
7; Conserva
                                                                                                               NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=P0470D12.115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=39947;
Richardson P.;
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                                                                                                                                  TISSUE=Embryo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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Matches
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WEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
REDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RIATAUSDERG R.L., Felingold B.A., Grouse L.H., Derge J.G.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haich F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J. Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rouffard G.G.,
A Hakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                               Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                Edwards M.R.,
"Cloning and expression of a prokaryotic enzyme, arginine deiminase,
from a primitive eukaryote Giardia intestinalis.";
J. Biol. Chem. 273:4470-4477(1998).
                                                                                                                                                                                                                       Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
0
                       STRAIN=Portland 1;
MEDLINE=98136144; PubMed=9468500; DOI=10.1074/jbc.273.8.4470;
Knodler L.A., Sekyere B.O., Stewart T.S., Schoffeld P.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Length 580;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                   580 AA; 64132 MW; 4812F389D0F5357A CRC64;
                                                                                                                                                                                                                                                                                                   BioCyc; MesaCyc: MONOMER-11205; -. GO, GO:0016990; F:arginine deiminase activity; IEA. GO; GO:0016787; F:hydrolase activity; IEA. FirsterPro; IPR03198; Amidino trans. Fem. PF02274; Amidino trans. Hydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2003, integrated into UniProtKB/TrEMBL 01-JUN-2003, sequence version 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         854 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ilarity 57.1%; Score 43; DB 57.1%; Pred. No. 44; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                    EMBL; U49236; AAC06116.1; -; Genomic_DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xenopodinae; Xenopus; Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       168 NNMVFMRDQQITTR 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 NNVLIQTDQQATTR 15
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    NUCLEOTIDE SEOUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
nes 8; Conserve
                                                                                                                                                                                                                                                                                            PIR; T45064; T45064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGC52979 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=8355;
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Q7ZXI4;
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SEQUENCE Query Match Matches

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Nubmed=15229592; DOI=10.1038/nature02579;

PubMed=15229592; DOI=10.1038/nature02579;

A Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,

Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla B.,

Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,

Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,

Boistame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,

A Bespons L., Fabre B., Fairhead C., Ferry-Dumazet H., Groppi A.,

Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,

Kerrest A., Koszul R., Lemaire M., Lesur I., Mal., Muller H.,

A Nicaud J.-M., Nikolski M., Oztar S., Ozier-Kalogeropoulos O.,

Pellenz S., Potier S., Richard G.-P., Straub M.-L., Suleau A.,

Zeniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,

Mincker C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,

Mincker P., Souciet J.-L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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O7-FEB-2006, entry version 3.

Chromosome 7 SCAF13760, whole genome shotgun sequence.

ORFNames=GSTENGG001200501;

Tetraodon nigroviridis (Green puffer).

Tetraodon nigroviridis (Green puffer).

Actinopterygii, Neopterygii; Teleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Candida glabrata (Yeast) (Torrlopsis glabrata).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             247 AA; 27274 MW; AEB540BB8B628D35 CRC64;
                                                                                                                                                                                                                                                 19-JUL-2004, sequence version 1.
07-FEBE-2006, entry version 11.
Similar to sp|P39721 Saccharomyces cerevisiae YAL049c.
OrderedLocusNames=CAGL0J07128g;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [1]
NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
                                                                                                                                                                                                     19-JUL-2004, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       integrated into UniProtKB/TrEMBL
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GO; GO:0016787; F:hydrolase activity; IEA.
InterPro; IPR002925; Dienelactn_hydro.
Pfam; PF01738; DLH; 1.
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Best Local Similarity
Matches 8; Conserv
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SEQUENCE 247 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=5478;
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                                                                                             QEFP28 CANGA
QEFP28;
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                                                           CANGA
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045VP5
TET 19-045VP5
AC 045VPF
AC 045VPF
AC 045VPF
DT 19-JU
DT 19-JU
DT 07-PE
DE CKPTOM
CO OKFVAM
COC BCHAR
COC ACTION
COC
RESULT 14

OG FP22

AC OG FP23

AC OG FP22

AC OG FP22

AC OG FP22

BD DT 19-JU

DT 19
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Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
Nicaud S., Jaffe D., Fischer S., Lutfalla G., Dossat C., Segurens B.,
Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
Bienont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
Artuaud C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J.,
Rellis M., Volff J.-N., Guigo R., Zody M.C., Mesirov J.-,
Lindblad-Toh K., Birren B., Nubbaum C., Rabin D., Robinson-Rechavi M.,
Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
Mincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
"Genome duplication in the teleost fish Tetraodon nigroviridis reveals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                            Genoscope; Whitehead Institute Centre for Genome Research;
Submitted (FBB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; CAAE01013760; CAF95377.1; -; Genomic DNA.
SEOUENCE 260 AA; 28404 MW; 7E3DC627AF6D41A2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55.4%; Score 41; DB 2; 70.0%; Pred. No. 42; iive 2; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 70...
To Conservative
                                                                                                                                                                                                                                                                                                               Nature 431:946-957(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    preliminary data.
                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE
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Search completed: August 30, 2006, 04:29:21 Job time : 61.4848 secs

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APPLICANT: Lawton. Robert
APPLICANT: Lawton. Robert
APPLICANT: Prancoeur, Greg
APPLICANT: Prancoeur, Greg
TITLE OF INVENTION: Specific Binding Protein for Treating
TITLE OF INVENTION: Canine Allergy
FILE REPREENCE: 01.1275A
CURRENT APPLICATION NUMBER: US/09/281,760E
CURRENT FILING DATE: 1999-03-30
PRIOR APPLICATION NUMBER: 09/058,331
PRIOR FILING DATE: 1998-04-09
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 37
LENGTH: 108
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 37, Application US/09281760E; Patent No. 6734287; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ||:: ||| |||
168 NNMVFMRDQQITTR 181
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Query Match
Best Local Similarity
Matches 8; Conserv
US-09-281-760E-37
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Sequence 2, Appli
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Sequence 2, Appli
Sequence 10, Appli
Sequence 10, Appl
Sequence 10, Appl
Sequence 18, Appl
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14, Appl

22, Appl

22386, A

22386, Ap

5969, Ap

408, App

408, App

301, App

301, App

301, App

301, App

301, App
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                                                                            August 30, 2006, 04:31:13 ; Search time 14.8485 Seconds (without alignments) 88.424 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                       Issued Patents AA:*
: / FMC Celerra SIDS3/ptodata/2/iaa/5 COMB.pep:*
: / EMC Celerra SIDS3/ptodata/2/iaa/6-COMB.pep:*
: / EMC Celerra SIDS3/ptodata/2/iaa/7-COMB.pep:*
: / EMC Celerra SIDS3/ptodata/2/iaa/H-COMB.pep:*
: / EMC Celerra SIDS3/ptodata/2/iaa/PCTUB.COMB.pep:*
: / EMC Celerra SIDS3/ptodata/2/iaa/RE COMB.pep:*
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           GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-09-281-760B-37

US-09-316-583-2

US-08-336-583-2

US-08-583-2

US-09-056-010-10

US-09-056-010-10

US-09-996-620-10

US-09-996-620-10

US-09-996-620-10

US-09-996-614-18

US-09-328-352-5826

US-09-479-614-2

US-09-479-614-2

US-09-248-796A-22386

US-09-248-796A-22386

US-09-248-796A-22386

US-09-248-796A-22386

US-09-283-310-4400

US-09-2010-433-5039

US-09-2010-431-5039

US-09-205-258-408

US-10-004-860-408
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US-09-997-333-301
US-09-992-598-301
US-09-989-735-301
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                                                                                                                                                                                                           650591 seqs, 87530628 residues
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                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                       - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Sequence 301, App
Sequence 24803, A
Sequence 1974, Ap
Sequence 1874, Ap
Sequence 18, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 118, Appl
Sequence 118, Appl
Sequence 102, Appl
Sequence 102, Appl
Sequence 102, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                             Sequence Sequence !
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-723-546-10

Sequence 10, Application US/09723546

Patent No. 6737259

GENERAL INFORMATION:
APPLICANT: Clark, Mike A

TITLE OF INVENTYON: Modified Arginine Deiminase
FILE REFERENCE: PHOE0059

CURRENT APPLICATION NUMBER: US/09/723,546

CURRENT APPLICATION NUMBER: 09/023,809

PRIOR APPLICATION NUMBER: 09/023,809

PRIOR FILING DATE: 1998-02-13

NUMBER OF SEQ ID NOS: 14

SOFTWARE PATENTIN Ver. 2.1

SEQ ID NO 10

LENGTH: S80

LYPE: PRT

ORGANISM: Qiardia intestinalis

US-09-723-546-10
                                                                          US-09-997-653-301
US-09-997-653-301
US-09-989-033A-8499
US-09-248-796A-24803
US-09-540-236-1974
US-09-107-532A-44821
US-09-107-532A-44821
US-09-134-001C-3544
US-09-134-01C-3544
US-09-138-188
US-09-198-188-185A-102
                                                                                                                                                                                                                                                                                                                      US-08-886-886-15
US-09-489-039A-12964
US-09-107-532A-5521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58.1%; Score 43; DB 2; ilarity 57.1%; Pred. No. 14; Conservative 2; Mismatches
                      US-09-997-514-301
US-09-989-728-301
US-09-997-349-301
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Gaps ö

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Score 41; DB 2; Length 312;
Pred. No. 16;
1; Mismatches 4; Indels
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Patent No. 5629415
GENERAL INFORMATION:
APPLICANT: HOLLIS, GREGORY F.
APPLICANT: PATEL, MAYUR D.
TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULIN E NUMBER OF SEQUENCES: 2
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: ALINCOLN AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 426;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 0705-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,583
FILING DATE: 09-NOV-1994
CLASSIFICATION: 424
ATTORNEY AGENT INFORMATION:
NAME: CARTY, CHRISTINE E.
REGISTRATION NUMBER: 36,099
REFREBROZE/DOCKET NUMBER: 19211
TELECOMMUNICATION INFORMATION:
TELEFAKX: (908) 594-6734
TELEFAKX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
FRACTH. 426 anino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 41; DB 1;
Pred. No. 23;
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                                   TYPE: PRT
ORGANISM: DOG
FEATURE:
OTHER INFORMATION: CH2CH3n of dog IGE
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55.4%;
                                                                                                                                                                                                                                                                                               55.4%;
64.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                         255 RNDSPIOTDOYTTT 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 RNNVLIQTDQQATT 14
                                                                                                                                                                                                                                                                                                                                                                                   1 RNNVLIQTDQQATT 14
                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 64...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 64.3
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein US-08-336-583-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 single
                                                                                                                                             AUTHORS: Patel,
JOURNAL: Immunogenetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRET: 12b L.
STREET: RAHWAY
CITY: RAHWAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: si:
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                                                                                                                                                                                   , VOLUME: 41
; PAGES: 282-286
; DATE: 1995
US-09-701-623C-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JS-08-336-583-2
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TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF
TITLE OF INVENTION: ALLERGY
FILE REPERENCE: 11514153US1
CURRENT APPLICATION NUMBER: US/09/701,623C
CURRENT FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: OFT/US/99/13959
PRIOR PELING DATE: 1999-06-21
PRIOR APPLICATION NUMBER: 09/100,287
PRIOR APPLICATION NUMBER: 09/100,287
PRIOR PELING DATE: 1998-06-20
NUMBER OF SEQ ID NOS: 91
SOFTWARE: PATENTI VET. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Pred. No. 4.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Indels
                   FEATURE:
NAME/KEY: misc_feature
NAME/KEY: (136)..(136)
OTHER INFORMATION: "n" stands for any nucleic acid
                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: misc_feature
LOCATION: (460)..(462)
OTHER INFORMATION: "n" stands for any nucleic acid
                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc feature
LOCATION: (500)..(500)
OTHER INFORMATION: "n" stands for any nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
MAME/KEY: misc feature
LOCALION: (568)..(568)
OTHER INFORMATION: "n" stands for any nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
MAMBIKEY: misc_feature
LOCATION: (847)..(849)
OTHER_INFORMATION: "n" stands for any nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc feature
LOCATION: (853)..(853)
OTHER INFORMATION: "n" stands for any nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (1382)..(1382).
OTHER INFORMATION: "n" stands for any nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature

// LOCATION: (1832)..(1832)

// OTHER INFORMATION: "n" stands for any nucleic acid

US-09-281-760E-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc feature
LOCATION: (530)..(530)
OTHER INFORMATION: "n" stands for any nucleic acid
                                                                                                                       NAME/KEY: misc feature
LOCATION: (413)..(414)
OTHER INFORMATION: "n" stands for any nucleic
                                                                                                                                                                                                         NAME/KEY: misc feature
LOCATION: (451)..(451)
OTHER INFORMATION: "n" stands for any nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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US-09-701-623C-2
; Sequence 2, Application US/09701623C
natent No. 6811/82
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ORGANISM: Canis familiaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 55.4
Best Local Similarity 64.3
Matches 9; Conservative
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LOCATION: (1382)..(138
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Gaps

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Shaw, Gray
Sako, Dianne
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           77 NOKLÍRKNÓGTÍTR 90
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261 RNEINVQSDVQAT 273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
                                                                                                                                                              US-09-026-001A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-026-001A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-996-620-10
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Patent No. 6703491

GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster: FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT APPLICATION NUMBER: US/09/270,767
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SSQ ID NO 41480
LENGTH: 345
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Pred. No. 23;
1; Mismatches 4; Indels
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GENERAL INFORMATION:
APPLICANT: HOLLIS, GREGORY F.
APPLICANT: PATEL, MAYUR D.
TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHRISTINE E. CARTY
STREET: 126 E. LINCOLN AVENUE; P.O. BOX 2000
                                                                                                                                                                                                                                                                                                                                CITY: RAHMAY
STATE: NEW JERGEY
COUNTRY: BUSINESS
CONFORTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: BY PC compatible
C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION:
ATTONEY/AGENT INFORMATION:
NAME: CARTY, CHRISTINE E.
REGISTRATION NUMBER: 36,099
REFERENCE/DOCKET NUMBER: 19211Y
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (908) 594-6734
TELEPHONE: (908) 594-4720
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 426 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55.4%;
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Best Local Similarity 64.37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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TITLE OF INVENTION: HIGHLY PURIFIED MOCARHAGIN, A COBRA VENOM PROTEASE, POLYNUCLEOTIDES ENCODING SAME AND RELATED PROTEAS THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                            APPLICANT: Boodhoo, Amechand
APPLICANT: Seehra, Jasbir
APPLICANT: Shaw, Gray
APPLICANT: ADDRESS: 22
CORRESPONDENCE ADDRESS: 22
CORRESPONDENCE ADDRESS: ADDRESSE: Genetics Institute, Inc.
STREET: Gambridge
STREET: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/026,001A
FILING DATE: 18-FEB-1998
CLASSIFICATION: 435
ATTONNEY/AGENT INFORMATION:
NAME: BICOM. SCOTE A.
REGISTRATION NUMBER: 32,724
REGISTRATION NUMBER: 32,724
REGISTRATION NUMBER: G15293B
TELEPHONE: (617) 499-8224
TELEPHONE: (617) 496-821
TELEPHONE: (617) 496-861
INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 38; DB 2; 1 Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
Sequence 10, Application US/09026001A, Patent No. 6413760, GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 10, Application US/09996620
Patent No. 6881404
GENERAL INFORMATION:
APPLICANT: Boodhoo, Amechand
Seehra, Jasbir
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US-09-996-620-18
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Patent No. 6413760

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Beochhoo, Jasbir
APPLICANT: Sahaw, Gray
APPLICANT: Sahaw, Gray
APPLICANT: SANAW, Dianne
TITLE OF INVENTION: THERAPEUTIC USES THEREOF
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                               ZIP: 02140

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/996,620
FILING DATE: 27-No. 6881404-2001
CLASSIFICATION: CURKNOWD.
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION TORRAHAIDM:
ATTORNEY/AGENT INFORMATION:
ANAMY. GENT INFORMATION:
ANA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER RELABBLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/026,001A
FILING DATE: 18-FEB-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G15293B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEPRAY: (617) 498-8224
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-996-620-10
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 613 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: <Unknown>
                                          CITY: Cambridge
STATE: Massachusetts
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261 RNEINVQSDVQAT 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
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US-09-026-001A-18
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TITLE OF INVENTION: HIGHLY PURIFIED MOCARHAGIN, A COBRA VENOM PROTEASE, POLYNUCLECTIDES ENCODING SAME AND RELATED PROTEAS THERAPEUTIC USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRIT APPLICATION DATE:

APPLICATION NUMBER: US/09/996,620

FILING DATE: 27-No. 6881404-2001
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                                                                                                                                                                                                                                                                                                                                                                        3; Indels
                                                                                                                                                                                                                                                                                                                      Score 38; DB 2;
Pred. No. 1.2e+02;
3; Mismatches 3
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STREET: 87 CambridgePark Drive
CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: GI5293B
TELECOMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-96-620-18
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APPLICATION UNDRER: 09/026,001
FILING DATE: 18-FEB-1998
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 32,724
REPRENCE/DOCKET NUMBER: G15293B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEPRAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE GIRARACTERISTICS:
LENGTH: 621 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Brown, Scott A. REGISTRATION NUMBER: 32,724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 18, Application US/09996620
Patent No. 6881404
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 621 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Boodhoo, Amechand
Seehra, Jasbir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 18:
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                                                                                                                                                                                                                                                                                                                        Query Match 51.4%;
Best Local Similarity 53.8%;
Matches 7; Conservative
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Sako, Dianne
                                                                                                                                                               LENGTH: 621 amino acids
TYPE: amino acid
STRANDEDNESS:
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CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                || : :|:| |||
269 RNEINVQSDVQAT 281
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                                                                                                                                                                                                                                  ; TOPOLOGY: linear; MOLECULE TYPE: protein US-09-026-001A-18
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Gaps

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US-09-248-796A-22386, Application US/09248796A

Sequence 2236, Application US/09248796A

Sequence 2236, Application US/09248796A

Sequence 2236, Application US/09248796A

Sequence 22386, Application US/09248796A

TITLE OF INVENTION: WOLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION NUMBER: US/09/248, 796A

CURRENT APPLICATION NUMBER: US 60/074,725

PRIOR PILING DATE: 1998-02-13

PRIOR PILING DATE: 1998-08-13

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 22386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NS-09-479-614-29

Sequence 29, Application US/09479614

Factor No. 65737-10.

Sequence 29, Application US/09479614

Factor No. 65737-10.

FAPLICANT: McCall, Catherine

APPLICANT: McCall, Catherine

FILE REFERENCE: P-1047

CURRENT FILING DATE: 2000-01-07

CURRENT FILING DATE: 2000-01-07

EARLIER APPLICATION NUMBER: 60/115,033

FARLIER FILING DATE: 1999-01-07

NUMBER OF SEQ ID NOS: 34

SOFTWARE: Patentin Ver. 2.0

SEQ ID NOS: 29
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Pred. No. 1.58+02;
2; Indels
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Pred. No. 1.5e+02;
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FILE REFERENCE: P-1047
CURRENT APPLICATION NUMBER: US/09/479,614
CURRENT FILING DATE: 2000-01-07
EARLIER APPLICATION NUMBER: 60/115,033
EARLIER FILING DATE: 1999-01-07
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: 496
                                                                                                                                                                                                                                                                                Query Match 50.0%;
Best Local Similarity 53.8%;
Matches 7; Conservative
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53.8%;
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428 NDSPVRTEQQATT 440
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428 NDSPVRTEQQATT 440
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Best Local Similarity 53.0
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                                                                                                                                                                                                                  ; ORGANISM: Felis catus US-09-479-614-2
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ORGANISM: Felis catus
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US-09-248-796A-22386
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                                                                                                                                                                                                             Sequence 5826, Application US/09328352

Patent No. 6562958

GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-06-04
CURRENT APPLICATION NUMBER: US/09/328,352
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 5826
LENGTH: 370
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Sequence 14, Application US/09479614

Sequence 14, Application US/09479614

Patcht No. 6573372

GENBEAL INFORMATION:

APPLICANT: Weber, Exic

TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods

FILE REFERENCE: P-1047

CURRENT APPLICATION NUMBER: US/09/479,614

CURRENT APPLICATION NUMBER: 60/115,033

EARLIER APPLICATION NUMBER: 60/115,033

MUMBER OF SEQ ID NOS: 34

SOFTWARE: Patchtin Ver. 2.0

SEQ ID NO 14

LENGTH: 431
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US-09-479-614-2
; Sequence 2, Application US/09479614
; Patent No. 6573372
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
                             Gaps
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                          3; Indels
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    Pred. No. 1.2e+02; 3; Mismatches 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Acinetobacter baumannii
    Best Local Similarity 53.8%;
Matches 7; Conservative
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175 KNNIVYTTDNSATS 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RNNVLIQTDQQATT 14
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                                                                                         Query Match
Best Local Similarity 42...
6; Conservative
                                                                1 RNNVLIQTDQQAT 13
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Matches 7; Conservative
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ORGANISM: Felis catus
                                                                                                                                                                                                US-09-328-352-5826
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Gaps

. 0 0; Gaps Query Match
48.6%; Score 36; DB 2; Length 153;
Best Local Similarity 77.8%; Pred. No. 57;
Matches 7; Conservative 0; Mismatches 2; Indels

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Search completed: August 30, 2006, 04:33:03 Job time : 15.8485 secs

us-10-758-165a-3.rapbm

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Sequence 3, Appli
Sequence 2, Appli
Sequence 30, Appli
Sequence 17, Appli
Sequence 17, Appli
Sequence 10, Appli
Sequence 12994, A
Sequence 129557,
Sequence 6713, Appli
Sequence 28, Appli
Sequence 28, Appli
Sequence 28, Appli
Sequence 181484,
Sequence 181484,
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10, Appl
23294, A
1, Appli
129557,
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138338,
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| SMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
| SMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
| SMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
| SMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
| SMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
| SMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
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                                                                                           August 30, 2006, 04:33:28; Search time 75.7576 Seconds (without alignments) 91.717 Million cell updates/sec
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Sequence
Sequence
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-451-078-2

US-10-451-078-4

US-10-214-524-30

US-10-052-788-4

US-10-052-788-4

US-10-75-843-10

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US-10-75-125-1

US-10-369-493-6713

US-10-123-181484

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US-10-123-181484

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US-10-13-181-181

US-10-14-52-18

US-11-066-236-10

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US-11-188-298-1274-8100

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US-11-1057-088-62

US-11-1057-088-62

US-11-1057-088-62
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                                                                                                                                                                                                                                                                                          2097797 seqs, 463214858 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                  OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length DB
                                                                                                                                                                   Title:
Perfect score:
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No.
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Sequence 587, App Sequence 14, Appl Sequence 14, Appl Sequence 2, Appli Sequence 29, Appli Sequence 29, Appli Sequence 29, Appli Sequence 1053, Ap Sequence 9730, Ap Sequence 313903, Sequence 31098, Sequence 310, Appl Sequence 29967, Sequence 2754, Ap Sequence 2754, Ap Sequence 2754, Ap	MALIAN SPECIES	Length 15; Indels 0; Gaps 0;	Encode the Constant Region of the Allotype, Recombinant ng Them, and Corresponding Antibodies and their Use
US-10-389-566-587 US-09-479-614-14 US-09-479-614-2 US-09-479-614-29 US-10-214-524-25 US-10-214-524-25 US-10-389-566-1053 US-10-389-566-1053 US-10-732-923-9730 US-10-732-923-9730 US-10-425-115-351098 US-10-128-714-8304 US-10-128-714-8304 US-10-24-237-2751 US-10-24-237-2751 US-10-24-237-2751 US-10-24-237-2751 US-10-24-237-2751 US-10-24-237-2751	RESULT 1 US-10-758-165-3 Sequence 3, Application US/10758165 Publication No. US20550196816A1 GENERAL INFORMATION: APPLICANT: Hammerberg, Bruce 1TITLE OF INVERTION: IMMUNOGLOBULIN E DETECTION IN MAWMALIAN SPECIES FILE REFERENCE: 5051-661 CURRENT APPLICATION NUMBER: US/10/758,165 CURRENT FILING DATE: 2004-01-16 PRIOR FILING DATE: 2003-01-16 PRIOR FILING DATE: 2003-01-16 SET OF FILING DATE: 2003-01-16 NUMBER OF SEQ ID NOS: 16 SOFTWARE: PATENTIN NOS: 16 SOFTWARE: PATENTIN VERSION 3.2 SEQ ID NO 3 INMUNICH: 15	. Score 74; DB 5; ; Pred. No. 2.5e-06; 0; Mismatches 0;	ic Acids which f an Equine 10F ns Obtained Usi fic Monoclonal 451,078
2 4 4 4 4 4 4 4 6 6 6 8 8 8 8 8 8 8 8 8 8	on US/107; 150196816A. 19, Bruce 10, WIMBER: UN 10, WIMBER: US 1003-01-16 1003-01-16	.0% .0% 15	SULT 2 -10-451-078-2 -10-451-078-2 -10-451-078-2 -10-451-078-2 -10-451-078-2 -10-451-078-2 -10-451-078-3 -10-10-10-10-10-10-10-10-10-10-10-10-10-
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	Applicati No. US200 NPMATION: Hammerber NUENTION: HIGHER NUENTION: NCE: 5051 NLICATION OU G DATE: CATION NU G DATE: CATI	Equus 3 imilaz ; Cor	ULT 2 10-451-078-2 10-451-078-2 10-451-078-2 UDLication No. US20040115764F ENERAL INPORMATION: APPLICANT: Leibold, Wolfgang APPLICANT: Betbold, Wolfgang APPLICANT: Radbruch, Andreas TITLE OF INVENTION: Heavy CI TITLE OF INVENTION: ISCYPO- TITLE OF INVENTION: ISCAPPO- TITLE OF INVENTION NUMBER: DE PRIOR FILING DATE: 2000-12-21 PRIOR FILING DATE: 2000-12-21 SOFTWARE: PATCHING DATE: 2000-12-21 SOFTWARE: PATCHING DATE: 2000-12-21
228 24 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	RESULT 1 US-10-758-165-3 Sequence 3, A Publication N GENERAL INFOR TITLE OF INV TITLE OF INV CURRENT FILI PRIOR PILING PRIOR APPLIC PRIOR FILING NUMBER OF SE SOFTWARE: Pa	$\alpha \Sigma \alpha \alpha \Delta$	RESULT 2 US-10-451-078-2 US-10-451-078-2 Publication No. US20 GENERAL INFORMATION: APPLICANT: Bettina, APPLICANT: Bettina, APPLICANT: Bettina, TITLE OF INVENTION: TIT
<u> </u>	RESULA US-10- 1 Seq. 1 Seq. 1 Cul. 1 TITI 1	T T C C US-10 Que Bes Mat	RESULT US-10- Sequence Publ Rebb APP TITT TITT TITT TITT TITT TITT TITT

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Sequence 30, Application US/10214524

; Sequence 30, Application US/10214524
; Publication No. US20030073142A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Swey-Shen Alex
; APPLICANT: Chen, Swey-Shen Alex
; APPLICANT: Barankiewicz, Theresa J.
; APPLICANT: Barankiewicz, Theresa J.
; APPLICANT: Chen, Zhong
; TITLE OF INVENTION: IMMUNOCIOBULIN E VACCINES AND METHODS OF USE THEREOF
; FILE REFERENCE: IGE-00101.P.1.1
; CURRENT APPLICATION NUMBER: US/10/214,524
; CURRENT FILING DATE: 2002-08-08
; PRIOR FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 61
; SEQ ID NO 30
; LENGTH: 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/10052788

| Sequence 4, Application US/10052788
| Publication No. US20030087314A1
| Publication No. US20030087314A1
| Publication No. US20030087314A1
| Publication No. US20030087314A1
| APPLICANT: Gershwin, Laurel J.
| APPLICANT: Fettigrew, Howard David
| APPLICANT: The Regents of the University of California
| TITLE OF INVENTION: Epsilon Immunoglobulin Chain Derived Peptides for TITLE OF INVENTION: Induction of Anti-IgE Antibodies
| FILE REFERENCE: O23070-121000US
| CURRENT APPLICATION NUMBER: US/10/052,788
| NUMBER OF SEQ ID NOS: 6
| SOFTWARE: PatentIn Ver. 2.1
| LENGTH: 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                    100.0%; Score 74; DB 4; Length 424; 100.0%; Pred. No. 0.00011;
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Pred. No. 0.00015;
                                                                    0; Mismatches
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ORGANISM: Horse (Equus caballus)
US-10-214-524-30
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Best Local Similarity 100.0%;
Matches 15; Conservative 0
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                    Query Match
Best Local Similarity 100.0
Matches 15; Conservative
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Sequence 4 Application US/10451078

Publication No. US20040115764A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Leibold, Wolfgang
APPLICANT: Bettina, Wagner
APPLICANT: Radbruch, Andreas
TITLE OF INVENTION: Decoyribonucleic Acids which Encode the Constant Region of the
TITLE OF INVENTION: Immunoglobulins Obtained Using Them, and Corresponding
TITLE OF INVENTION: Immunoglobulins Obtained Using Them, and Corresponding
TITLE OF INVENTION: Isotype-specific Monoclonal Antibodies and their Use
FILE REFERENCE: 03100177a
CURRENT APPLICATION NUMBER: US/10/451,078

CURRENT APPLICATION NUMBER: DE7/DE01/04810

PRIOR FILING DATE: 2000-12-24

PRIOR FILING DATE: 2000-12-21

NUMBER OF SEQ ID NOS: 7

SOFTWARE: Patentin version 3.2

SEQ ID NO 4

LENTH: 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 74; DB 4; I
100.0%; Pred. No. 0.00011;
                                                                                           FEATURE:
NAME/KEY: Domain
LOCATION: (1)..(97)
OTHER INFORMATION: CHI domain, IGE allotype a
                                                                                                                                                                                                                                                                                                            NAME/KEY: Domain
LOCATION: (206)...(312)
OTHER INFORMATION: CH3 domain, IgE allotype a
                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: Domain

LOCATION: (313)...(424)

OTHER INFORMATION: CH4 domain, IGE allotype a

US-10-451-078-2
                                                                                                                                                                                                                                           LOCATION: (98)...(205)
OTHER INFORMATION: CH2 domain, IgE allotype a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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LOCATION: (206)...(312)
OTHER INFORMATION: CH3 domain, IgE allotype
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NAME/KEY: Domain
LOCATION: (313)..(424)
CTHER INFORMATION: CH4 domain, IgE allotype
US-10-451-078-4
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OTHER INFORMATION: CH2 domain, IgE allotype
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OTHER INFORMATION: CH1 domain, IgE allotype
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0
Matches 15, Conservative
                                             TYPE: PRT
ORGANISM: Equus caballus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Equus caballus
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NAME/KEY: Domain
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NAME/KEY: Domain
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LOCATION: (98)...
SEQ ID NO 2
LENGTH: 424
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                                                                                                             Sequence 17, Application US/10674666
; Publication No. US20040131604A1
; GENERAL INFORMATION:
; APPLICANT: Clark, Mike A.;
; TITLE OF INVENTION: Methods for Inhibiting Viral Replication in vivo
; FILE REFERENCE: PHOE0001-100
; CURRENT FPLICATION NUMBER: US/10/674,666
; CURRENT FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: US 60/427,497
; RIOR APPLICATION NUMBER: US
; SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 580
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US-10-732-923-2394

US-10-732-923-2394, Application US/10732923

Sequence 23294, Application US/10732923

Publication No. US20050108791A1

GENERAL INFORMATION:

APPLICANT: Edgerton, Michael D

TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES

FILE REPREBLICE: 38-15(52796)C

CURRENT APPLICATION NUMBER: US/10/732,923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 43; DB 4; Length 580;
Pred. No. 59;
2; Mismatches 4; Indels
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Pred. No. 59;
2; Mismatches 4; Indels
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TITLE OF INVENTION: Modified Arginine Deiminase
FILE REFERENCE: PHOSO059
CURRENT APPLICATION NUMBER: US/10/757,843
CURRENT FILING DATE: 2004-01-15
PRIOR APPLICATION NUMBER: US/09/723,546
PRIOR APPLICATION NUMBER: 0S/023,809
PRIOR FILING DATE: 1998-02-13
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 10, Application US/10757843; Publication No. US20050129706A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Giardia intestinalis
US-10-674-666-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Qiardia intestinalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 58.1%;
Best Local Similarity 57.1%;
Matches 8; Conservative ;
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Best Local Similarity 57.1%;
Matches 8; Conservative
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168 NNMVFMRDQQITTR 181
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168 NNMVFMRDQQITTR 181
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||||||||||||||||IQTDQQATTR 10
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US-10-674-666-17
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LENGTH: 580
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APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: APLICANT: APLANT Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Plantes and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: 19-10/32210 B
CURRENT FILING DATE: 2003-05-14
CURRENT FILING DATE: 2003-05-14
SEQ ID NO 129557
LENGTH: 105
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                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1. Application US/10788165

Sublication No. US20050196816A1

GENERAL INFORMATION:

APPLICATY: Hammerberg, Bruce

TITLE OF INVERTION:

FILE REFERENCE: 5051-661

CURRENT APPLICATION NUMBER: US/10/758,165

CURRENT APPLICATION NUMBER: US/04/01-16

PRIOR FILING DATE: 2003-01-16

NUMBER OF SEQ ID NOS: 16

SOFTWARE: Patentin version 3.2

SOFTWARE: Patentin version 3.2
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Pred. No. 1.7e+02;
0; Mismatches 2; Indels 1
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Pred. No. 2.2;
1; Mismatches
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CURRENT FILING DATE: 2003-12-10
PRIOR APPLICATION NUMBER: 10/310,154
PRIOR FILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 24149
SEQ ID NO 22294
LENGTH: 854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55.4%;
                                                                                                                                                                                                           Query Match 56.1%;
Best Local Similarity 78.6%;
Matches 11; Conservative
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Best Local Similarity 64.3%,
Best Local 9; Conservative
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                                                                                                                                               ; ORGANISM: Xenopus laevis
US-10-732-923-23294
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ORGANISM: Oryza sativa
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; VOLUME: 41
; PAGES: 282-286
; DATE: 1995
US-10-723-207-2
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REPERENCE: 38-10 (52052)8
CURRENT FILING DATE: 2003-02-28
PRIOR PILING DATE: 2003-02-28
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 6713
LENGTH: 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/10723207

Sequence 2, Application US/10723207

Publication No. US20050250934A1

GENERAL INFORMATION:

JAPPLICANT: Wang, Chang Yi

APPLICANT: Walfield, Alan M.

TITLE OF INVENTION: PLERGY

FILE REFERENCE: 1151-4153G2

CURRENT FILING DATE: 2003-11-24

PRIOR APPLICATION NUMBER: US/10/723,207

CURRENT FILING DATE: 2000-12-01

PRIOR PILING DATE: 1999-06-20

PRIOR APPLICATION NUMBER: PCT/US99/13959

PRIOR FILING DATE: 1998-06-20

PRIOR APPLICATION NUMBER: 09/100,287

PRIOR APPLICATION NUMBER: 09/100,287

PRIOR PILING DATE: 1998-06-20

NUMBER OF SEQ ID NOS: 91

SEQ ID NO 2

LENGTH 312

LENGTH 312
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Pred. No. 67;
3; Mismatches 3; Indels
                    DB 4; Length 105;
                                                                               2; Indels
                                       55.4%; Score 41; DB 46.7%; Pred. No. 20; Live 6; Mismatches
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PUBLICATION INFORMATION:
AUTHGRS: Patel,
JOURNAL: Immunogenetics
                                                                                                                                                                                                                                                             Sequence 6713, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Caenorhabditis elegans US-10-369-493-6713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55.4%;
                                                                                                                       1 RNNVLIQTDQQATTR 15
                                                                                                                                              10 RNNGVMELEEQATSR 24
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159 DNVLIQKDEENTAR 172
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                                   Query Match
Best Local Similarity 46.7
Matches 7; Conservative
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Matches 8; Conservative
  US-10-437-963-129557
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ORGANISM:
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US-10-214-524-28

US-10-214-524-28

Sequence 28, Application US/10214524

Publication No. US20030073142A1

GENERAL INFORMATION:

APPLICANT: Yang, Yong-Min

APPLICANT: Yang, Yong-Min

APPLICANT: Chen, Swey-Shen Alex

APPLICANT: Chen, Shong

ITILE OP INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF

FILE REFERENCE: IGE-00101.P.1.1

CURRENT APPLICATION NUMBER: 2002-08-08

PRIOR APPLICATION NUMBER: 60/312,120

PRIOR APPLICATION NUMBER: 60/312,120

PRIOR SED ID NOS: 61

SOFTWARE: Patentin version 3.1

SEQ ID NO 28

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   Length 312;
                                 4; Indels
Score 41; DB 5;
Pred. No. 67;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: unsure
LOCATION: (1)..(917)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Dog (Canis familiaris)
US-10-214-524-28
 Query Match 55.4%;
Best Local Similarity 64.3%;
Matches 9; Conservative
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                                                                                              255 RNDSPIOTDOYTTT 268
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                                                              1 RNNVLIOTDOOATT 14
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; Sequence 7, Application US/10758165
; Publication No. US2005019681641
; GENERAL INFORMATION:
; APPLICANT: Hammarberg, Bruce
; TITLE OF INVENTION: IMMUNGGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; TILE REPERENCE: 5051-661
; CURRENT PAPLICATION NUMBER: US/10/758,165
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 7
                                                                                                                                         0; Gaps
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                                                                                     Query Match 55.4%; Score 41; DB 4; Length 917; Best Local Similarity 50.0%; Pred. No. 2.3e+02; Matches 7; Conservative 3; Mismatches 4; Indels
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Best Local Similarity 46.7%; Pred. No. 3.3;
Matches 7; Conservative 4; Mismatches 4; Indels
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_78753C.1.pep
US-10-437-963-181484
                                                                                                                                                                                                           1 RNNVLIQTDOOATTR 15
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; TYPE: PRT
; ORGANISM: Sus scrofa
US-10-758-165-7
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US-10-758-165-7
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Search completed: August 30, 2006, 05:13:02 Job time: 76.7576 secs

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711337, A 288237, A 694609, Ap 694609, Ap 669609, A 861118, A 712348, A 712348, A 72244, A 72244, A 72244, A 72243, A 72243, A 72243, A 72243, A 72243, A 72263, A 72263, A 72263, A

Perfect score:

9

Sequence:

Scoring table:

Searched:

Minimum DB Maximum DB

Database

Result

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APPLICANT: Dumas Milne Edwards, Jean Baptiste
APPLICANT: Dumas Milne Edwards, Jean Baptiste
APPLICANT: Bougueleret, Lydie
FILLE REPERENCE: 78.054.CIP
CURRENT APPLICATION NUMBER: US/11/197,712
CURRENT FILLNG DATE: 2005-08-04
PRIOR APPLICATION NUMBER: US/09/876,997
PRIOR FILLNG DATE: 2001-06-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 40097, Application US/10449902
; bublication No. US20060123505A1
; bublication No. US20060123505A1
; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FOUNDATION:
FILE REFERENCE: MOA-A0205Y1-US
CURRENT FILING DATE: 2003-05-29
PRIOR FILING DATE: 2003-05-29
PRIOR FILING DATE: 2002-05-30
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 40987
Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Seq
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                                                             US-11-056-355B-69409
US-11-056-355B-69694
US-11-056-355B-61137
US-11-056-355B-6118
US-11-056-355B-69408
US-11-056-355B-69693
US-11-056-355B-72244
US-11-056-355B-72244
US-11-056-355B-72244
US-11-056-355B-72243
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Mismatches
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Publication No. US20060130160A1
GENERAL INFORMATION:
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144 KUNIMVILDNOMTT 157
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; ORGANISM: Oryza sativa
US-10-449-902-40987
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Best Local Similarity
US-10-449-902-40987
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11994', Ap
11994', Ap
11998', Ap
11937', Ap
11937', Ap
11937', Ap
11997', Ap
                                                                                                                                                                                   (without alignments)
133.695 Million cell updates/sec
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1. /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

2. /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

3. /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

4. /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

5. /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

6. /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

7. /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

7. /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

8. /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US00_NEW_PUB.pep:*
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                                                                                                                                                             August 30, 2006, 04:34:57; Search time 7.72727 Seconds
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                      GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-11-30-40-2292

US-11-30-40-2292

US-11-056-355B-23703

US-11-056-355B-23703

US-11-056-355B-8177

US-11-056-355B-8177

US-11-056-355B-8177

US-11-056-355B-8177

US-11-056-355B-8177

US-11-056-355B-23701

US-10-953-349-1097

US-11-056-355B-43156

US-11-056-355B-43156

US-11-056-355B-43176

US-11-056-355B-8176

US-11-056-355B-105308

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US-11-056-355B-105308
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                   OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Gaps

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APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
TITLE OF INVENTION: ENCONDED THERBY
TITLE OF INVENTION: ENCONDED THERBY
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PATENTIN version 3.3
SEQ ID NO 1098
LENGTH: 240
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Sequence 23703, Application US/11056355B

Publication No. US20060150283A1

GENERAL INFORMATION:
APPLICANT: Brover, Vyacheslav
APPLICANT: Brover, Vyacheslav
APPLICANT: Brover, Wickolai
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENCE: 2750-1550PUS2
CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2005-02-14
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR APPLICATION NUMBER: 60/544,190
SEQ ID NOS: 119966
SEQ ID NOS: 119966
SEQ ID NOS: 12996
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      Indels
      4,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 47.3%; Score 35; DB 7;
Best Local Similarity 50.0%; Pred. No. 39;
Matches 7; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LOCATION: (1)...(233)
; OTHER INFORMATION: Ceres Seq. ID no. 13487886
US-11-056-3558-23703
      Mismatches
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Publication No. US20060107345A1
GENERAL INFORMATION:
    3;
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ORGANISM: Arabidopsis thaliana
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US-10-953-349-1098
                                                                | ||::: | |||
195 RQNVVVELVQAATT 208
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                                             1 RNNVLIQTDQQATT 14
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11 NNIVLKLDQASTS 23
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      7; Conservative
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: peptide
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      Matches
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Sequence 1194, Application US/10953349

Publication No. US20060107345A1

GENERAL INFORMATION:

TAPPLICANT: ALEXANDROW, NickOLDE tal.

TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

TITLE OF INVENTION: ENCONDED THERBY

FILE REFERENCE: 2750-1579PUS2

CURRENT FILING DATE: 2004-09-30

NUMBER OF SEQ ID NOS: 40252

SOFTWARE: Patentin version 3.3

SEQ ID NO 1194

LENGTH: 223
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Pred. No. 39;
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Pred. No. 77;
2; Mismatches 0; Indels
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TITLE OF INVENTION: Genes and Uses for Plant Improvement FILE REPERENCE: 38-21(53529)B
CURRENT APPLICATION NUMBER: US/11/330,403
CURRENT FILING DATE: 2006-01-12
SEQ ID NOS: 19250
LENGTH: 585
                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
PRIOR APPLICATION NUMBER: US 09/731,872
PRIOR FILING DATE: 2000-12-07
PRIOR PILING DATE: 2000-12-07
PRIOR PILING DATE: 2000-03-06
PRIOR PILING DATE: 2000-03-06
PRIOR PILING DATE: 1999-12-08
NUMBER OF SEQ ID NOS: 482
SOFTWARE: Patent.pm
SEQ ID NO 247
LENGTH: 348
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Pred. No.
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US-11-330-403-2292
; Sequence 2292, Application US/11330403
; Publication No. US20060159563A1
; GENERAL INFORMATION:
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ORGANISM: Arabidopsis thaliana
US-10-953-349-1194
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50.0%;
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Best Local Similarity 75.0%;
Matches 6; Conservative 5
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Best Local Similarity 53.5-
Transfer Conservative
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Best Local Similarity
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LOCATION: -29..-1
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RESULT 11

US-10-953-349-1192

US-10-953-349-1192

Sequence 1192, Application US/10953349

Publication No. US20060107345A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
TITLE OF INVENTION: US/10/953,349

CURRENT APPLICATION UNDBER: US/10/953,349

CURRENT APPLICATION UNDBER: US/10/953,349

CURRENT APPLICATION OF SEQ ID NOS: 40252

NUMBER OF SEQ ID NOS: 40252

SOFTWARE: PATENTIN VERSION 3.3

SEQ ID NO 1192

LENGTH: 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Brover, Vyacheslav
APPLICANT: Alexandrov, Nickolai
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENCE: 2750-1590PUS2
CURRENT EPPLICATION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2004-02-14
PRIOR FILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
SEQ ID NO 23702
LENGTH: 317
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Pred. No. 59;
3; Mismatches 4; Indels
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Pred. No. 59;
3; Mismatches
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| LOCATION: (1)..(317)
| OTHER INFORMATION: Ceres Seq. ID no. 13487885
| US-11-056-3558-23702
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF EEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 1193
LENGTH: 317
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 23702, Application US/11056355B Publication No. US20060150283A1 GENERAL INFORMATION:
                                                                                                                                                         ; ORGANISM: Arabidopsis thaliana US-10-953-349-1193
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ORGANISM: Arabidopsis thaliana
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Best Local Similarity 50.0%;
Matches 7; Conservative
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Best Local Similarity 50.0%;
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289 RONVVVELVQAATT 302
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Publication No. US20060107345A1

GRNERAL INFORMATION:

APPLICANT: ALEXANDROV, Nickolai et al.

TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

TITLE OF INVENTION: ENCONDED THERBY

FILE REPERENCE: 2750-15799US2
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Sequence 85177, Application US/11056355B

Publication No. US20060150283A1

GENERAL INFORMATION:
APPLICANT: Brover, Vyacheslav

APPLICANT: Alexandrov, Nickolai

TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENCE: 2750-1590PUS2

CURRENT APPLICATION NUMBER: US/11/056,355B

CURRENT PILING DATE: 2005-02-14

PRIOR APPLICATION NUMBER: 60/544,190

PRIOR FILING DATE: 2004-02-13

NUMBER OF SEQ ID NOS: 119966

SEQ ID NO 85177
                APPLICANT: Brover, Vyacheslav
APPLICANT: Alexandrov, Nickolai
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENCE: 2750-1590F052
CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2005-02-14
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR PILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
SEQ ID NO 41157
LENGTH: 240
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Pred. No. 42;
6; Mismatches 2; Indels
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Pred. No. 42;
6; Mismatches
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| LOCATION: (1)..(240)

| OTHER INFORMATION: Ceres Seq. ID no. 12679238

US-11-056-3358-85177
                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: peptide
LOCATION: (1)..(240)
OTHER INFORMATION: Ceres Seq. ID no. 13487787
                                                                                                                                                                                                                                                                                                 TYPE: prt
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: prt
ORGANISM: Arabidopsis thaliana
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38.5%;
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11 NNIVLKLDQASTS 23
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11 NNIVLKLDQASTS 23
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Best Local Similarity 38.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 38.5
Matches 5; Conservative
         GENERAL INFORMATION:
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US-10-953-349-1193
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GENERAL INFORMATION:

APPLICANT: Brover, Vyacheslav

APPLICANT: Alexandrov, Nickolai

TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding

TITLE OF INVENTION: Polypeptides Encoded Thereby

TITLE OF INVENTION: Polypeptides Encoded Thereby

TITLE OF INVENTION: Polypeptides Encoded Thereby

FILE REFERENCE: 2750-1590FUS2

CURRENT APPLICATION NUMBER: US/11/056,355B

CURRENT FILING DATE: 2005-02-14

PRIOR APPLICATION NUMBER: 60/544,190

NUMBER OF SEQ ID NOS: 119966

SEQ ID NO 43156

LENGTH: 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 35; DB 7;
Pred. No. 79;
6; Mismatches 2
                                                                                                                                                                                                                                                                                                                                               | NAME/KEY: peptide
| LOCATION: (1)..(409)
| OTHER INFORMATION: Ceres Seq. ID no. 13487786
| US-11-056-3558-43156
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ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                      TYPE: prt
ORGANISM: Arabidopsis thaliana
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Publication No. US20060150283A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 38.5%;
Matches 5; Conservative
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180 NNIVLKLDOASTS 192
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Best Local Similarity 38.5.
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Publication No. US20060107345A1
GENERAL INFORMATION:
GENERAL INFORMATION:
THE OF INVENTION: SEQUENCE-DETERNINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION VMDER: US/10/953,349
CURRENT APPLICATION VMDER: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 1097
                                                                                                                                                                                        Sequence 23701, Application US/11056355B
; Publication No. US20060150283A1
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Brover, Vyacheslav
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypetides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 23701
: LENGTH: 388
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Pred. No. 79;
6; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 388;
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                     4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 35; DB 7;
Pred. No. 74;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; LOCATION: [1]..(388)
; OTHER INFORMATION: Ceres Seq. ID no. 13487884
US-11-056-3558-23701
Pred. No. 74;
3; Mismatches
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US-11-056-355B-43156
; Sequence 43156, Application US/11056355B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-1097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: prt
ORGANISM: Arabidopsis thaliana
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Best Local Similarity 50.0%;
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50.0%;
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ilarity 38.5%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: peptide
                                                                                                                                                               RESULT 12
US-11-056-355B-23701
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Gaps

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Length 409; 2; Indels

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                                                                    APPLICANT: Brover, Vyacheslav
APPLICANT: Brover, Vyacheslav
APPLICANT: Alexandrov, Nickolai
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENCE: 2750-1590PUS2
CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2005-02-14
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR FILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
SEQ ID NO 85176
LENGTH: 409
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Pred. No. 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 | FEATURE:
| NAME/KEY: peptide
| LOCATION: (1)..(409)
| THER INFORMATION: Ceres Seq. ID no. 12679237
| US-11-056-3558-85176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Mismatches
Sequence 85176, Application US/11056355B Publication No. US20060150283A1 GENERAL INFORMATION:
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August 30, 2006, 04:15:52 ; Search time 65.4545 Seconds (without alignments) 125.735 Million cell updates/sec Run on:

1 VDGQKATNIFPYTAPGTK 18 US-10-758-165A-9 97 Perfect score:

Scoring table:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

2589679 Total number of hits satisfying chosen parameters:

2589679 seqs, 457216429 residues

Searched:

seq length: 0 seq length: 200000000 88 08 08 Minimum I Maximum I

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* geneseqp2006s:* geneseqp2001s:* geneseqp2002s:* geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2005s:* Genesed 8: Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Adr10609 Dog 1gE e			Aar97753 Canine Ig	Abp96583 Dog IgE h	Cat	Adg73237 Cat immun	Abp96580 Cat IgE h	Feli	Abu09336 Feline Ig	Cat	_	Duc	Aab06204 Platypus	Adf90022 Opossum-r	Adn00643 ORO prote	Adf90025 Opossum-h	Adn00646 OSO prote	Aab06206 Immunogen	Aab03644 Opossum I	Aab06208 Immunogen	Aab06205 Immunogen	Aab06207 Immunogen
SUMMARIES	ΩI	ADR10609	AAY79995	AAW23067	AAR97753	ABP96583	ADR10610	ADG73237	ABP96580	ABU09338	ABU09336	ADG73251	ADG73225	ABP96584	AAB06204	ADF90022	ADN00643	ADF90025	ADN00646	AAB06206	AAB03644	AAB06208	AAB06205	AAB06207
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dŧ	Query Match	100.0	100.0	100.0	100.0	100.0	89.7	89.7	89.7	89.7	89.7	89.7	89.7	75.3	70.1	59.8	59.8	59.8	59.8		59.8	59.8	59.8	59.8
	Score	97	97	97	97	97	87	87	87	87	87	87	87	73	68	58	58	58	28	58	28	28	28	28
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Adf90033 Opossum-h Adn00654 OSO-H pro Adn00661 H-OCO-H p Abn96591 Brushtail				Adr10612 Sheep IgE Abp96588 Pig IgE h Aab06202 Immunogen Aab06201 Immunogen	Aay76530 Human ova Abo81258 Pseudomon Adu00341 Iron hydr
ADF90033 ADN00654 ADN00661 ABP96591	ABP96587 ADF90027 ADN00648	ADF90035 ADN00656 ADN00652	ADF90029 ADF90037 ADN00658 ADN00650	ADR10612 ABP96588 AAB06202 AAB06201	AAY76530 ABO81258 ADU00341
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ALIGNMENTS

Antiasthmatic; Antiallergic; Immunosuppressive; IgE; dog; asthma; anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody. Dog IgE epitope recognised by monoclonal antibody 3.76, SEQ ID 9. ADR10609 standard; peptide; 18 AA. (UYNC-) UNIV NORTH CAROLINA STATE. 15-JAN-2004; 2004WO-US003566. 16-JAN-2003; 2003US-0440472P. 21-OCT-2004 (first entry) Canis familiaris. WO2004065936-A2. Hammerberg B; 05-AUG-2004. ADR10609; RESULT 1

WPI; 2004-593545/57.

Novel antibody that specifically binds to mammalian IgE epitope, useful for testing an allergen reactivity of IgE sample, detecting mammalian IgE or treating asthma or anaphylactic shock.

Example 6; Page 9; 14pp; English.

The present invention relates to a novel monoclonal antibody (I) that specifically binds to a mammalian IgE epitope, where the epitope is between amino acids 145-166 or 356-374 of mammalian IgE, e.g. dog IgE. (I) is useful for testing an allergen reactivity of an IgE sample. The allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut and corn allergens. The sample is a biological sample collected from a dog, cat or horse. (I) is also useful for detecting mammalian IgE and for treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal antibodies recognise epitopes on canine IgE corresponding to amino acid residues 357-371 (ADR10601) and 146-162 (ADR10609) respectively of the canine IgE epsilon-chain. Recognition of epsilon-chains from IgE from

Pred. No. 1.3e-07;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           maximize cross-reactivity to the natural target. They induce safe (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino acid
                 3.76 were observed to have good cross-reactivity with the epsilon-chain of IgE from cat and horse, but did not exhibit cross-reactivity with either pig or human epsilon-chains of IgE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen; immunogenic; immunostimulatory; carrier protein; helper T cell epitope; antibody; allergy; allergic disease; immunisation; anti-allergic; anti-asthmatic; asthma; anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antigenic peptide from the CH3 domain of immunoglobulin E, fusions immunization against allergy.
    horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and
                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes immunoglobulin E (IgE)-CH3 domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               anaphylactogenic) antibodies. AAY79994 to AAY80084 represent a sequences used in the exemplification of the present invention
                                                                                                                                               100.0%; Score 97; DB 8; Length 18; 100.0%; Pred. No. 6.5e-09; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dog immunoglobulin E epsilon heavy chain SEQ ID NO:2.
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                                                                                                                                                                                                                                                                                                                                                                                AAY79995 standard; protein; 312 AA.
                                                                                                                                                                                                                                  1 VDGQKATNIFPYTAPGTK 18
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Les 18; Conservative
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                                                                                                          Sequence 18 AA;
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100.0%; Score 97; DB 3; Length 312;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This polypeptide is encoded by exons 1-4 (see AAT79278) of canine IgE heavy chain constant region (epsilon) genomic DNA. Another polypeptide, comprising the exon 5 and 6 product, is given in AAW23068. Recombinant peptides encoded by exons 1-6 can be produced in eukaryotic or prokazyotic cells. Such peptides, and antichodies raised against them, are used in methods to treat the manifestation of allergy in dogs, e.g. to treat Type I immediate hypersensitivity, and for immunomodulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        canine IgE heavy chain constant region DNA - useful to develop for treatment of canine allergies and for immunomodulation in
Gaps
                                                                                                                                                                                                                    IgE; immunoglobulin; antibody; heavy chain constant region; allergy; hypersensitivity; therapy; dog; antisense; immunomodulation.
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                                                                                                                                                                                                Canine IgE heavy chain constant region (exon 1-4 product).
Indels
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                                                                                                       AAW23067 standard; protein; 417 AA.
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                                    48 VDGQKATNIFPYTAPGTK
                     1 VDGQKATNIFPYTAPGTK
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1997-425031/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference 176
                                                                                                                                                                                                                                                                                                                                        67
                                                                                                                                                                                                                                                        Canis familiaris
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16-JUN-2005
19-FEB-1998
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The present invention describes a method (MI) for identifying peptides that induce cytotoxic T-lymphocyte (CTL) response against immunoglobulin E [19], comprising providing a test peptide (T) suspected of being able to bind to major histocompatibility complex (MHC) class I molecule, and evaluating (T) for ability to elicit in a mammal a CTL response to naturally processed and presented IgE peptides, where a peptide that induces such a response is identified. Also described are compositions: (C1) comprising at least one immunogenic peptide (I) identified by (MI); (C2) comprising at least one isolated polymiclecitide encoding (I); and (C3) comprising antigen-presenting cells that recognise at least one (I). Where (I-3 are able to bind to at least one MHC class I molecule and to elicit in a mammal a CTL response to naturally processed and presented cells; in a mammal a CTL response to naturally processed and presented cells peptides. C1-3 have antiallargic, antiasthmatic, immunosuppressive, vasotropic, dermatological, antiallammatory and cytostatic activities, and can be used as inducers of a CTL response against IgE, and in vaccines. C1-3 can be used for modulating an IgE-mediated condition in a mammal. C1-3 are useful for modulating an IgE-mediated condition in a mammal. The mediated atopic of hypersensity in a mammal because it is a mammal of the presence of a CTL response against IgE-mediated on-acpoic the mediated in a mammal of the mediated on-acpoic to the mediated in a mammal of the mediated on the mediated on-acpoic to the mediated in a mammal of the mediated in a mammal of the mediated on a mammal of the mediated on the mediated on-acpoic to the mediated in a mammal of the mediated on the mediated on-acpoic to the mediated in a mammal of the mediated on-acpoic to the mediated in the mediated on-acpoic to the mediated in the mediated on-acpoic to the mediated in the mediated on account of the mediated on the mediated on-acpoic to the mediated in the mediated on-acpoic to the mediated on account of the med
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying peptides that induce cytotoxic T-lymphocyte, CTL response against IgE, by identifying peptide eliciting CTL response to IgE peptides naturally presented by major histocompatibility complex class I
                                                                                                                                                                           Immunoglobulin B; vaccine; IgE; cytotoxic T lymphocyte response; immuno response; major histocompatibility complex; MHC; immunogenic; antiallergic; antiasthmatic; immunosupressive; vasotropic; cytostatic; dermatological; antiinflammatory; IgE-mediated condition; food allergy; atopic hypersensitivity condition; allergic rhinitis; allergic asthma; atopic dermatitis; non-atopic hypersensitivity condition; anaphylaxis;
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                                                                                                                            Dog IgE heavy chain amino acid sequence SEQ ID NO:28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chen Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 7; Page 152-154; 187pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Barankiewicz T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        146 VDGQKATNIFPYTAPGTK 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 VDGQKATNIFPYTAPGTK 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-AUG-2002; 2002WO-US026986.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-AUG-2001; 2001US-0312120P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (IGET-) IGE THERAPEUTICS INC
                                                                         28-MAY-2003 (first entry)
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Best Local Similarity
Matches 18; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                         Canis familiaris.
                                                                                                                                                                                                                                                                                                                                           urticaria hives.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             WO2003015716-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chen SA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              isolated gene (AAT29824) obtd. from a canine liver DNA library. The cloning of the IgB gene allows prodn. of large quantities of recombinant IgB using bacterial, yeast, mammalian, insect or viral systems. The IgB can be used in drug development (e.g. small molecule screening, assay development and anti-IgB antibody generation). Fragments of IgB can be used in vaccines or to prevent IgB-mediated hypersensitivity. The new sequence information permits targeted modulation of IgB-mediated immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New DNA encoding canine IgE and IgA - useful in vaccines, anti-sense therapy, assays, drug screening, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lgE; immunoglobulin; antibody; vaccine; allergy; hypersensitivity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              canine IgE amino acid sequence (AAR97753) was deduced from an
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                                                                                                                            100.0%; Score 97; DB 2; Length 417;
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                     Revised record issued on 30-JUN-2005 : Typo in comments
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                                                                                                                                                  1.8e-07;
                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                 AAR97753 standard; protein; 426 AA.
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                                                                                                                                                                                                                                                                 141 VDGQKATNIFPYTAPGTK 158
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                                                                                                                                                     100.0%;
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                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1996-277321/28.
                                                                                                                                                  Local Similarity
nes 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Canis familiaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAT29824
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                                                                            Sequence 417 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-MAY-1996.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Canine IgE
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RESULT 5 ABP96583 ID ABP9

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The invention describes an isolated nucleic acid molecule (I) encoding a portion of a feline IgE heavy chain protein. The methods and compositions of the present invention are useful for eliciting feline immune responses for and/or treating IGE-mediated responses, such as allergies. This is the amino acid sequence of a cat immunoglobulin E (IgE) constant region.
                                                                                                                                                                                                                                                                                                                                                                                                                                     heavy chain protein, useful for treating and/or eliciting feline immune responses for IGB-mediated responses, such as allergies.
                                antiallergic; IgE-modulator; vaccine; feline; IgE; immunoglobulin E; immune response; IgE-mediated response; allergy; cat; constant region.
                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated nucleic acid molecule encoding a portion of a feline IgE heavy chain protein, useful for treating and/or eliciting feline immur
Cat immunoglobulin E (IgE) constant region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 12; SEQ ID NO 14; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABP96580 standard; protein; 496 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         151 VDĞQKATNIFPYTAPG 166
                                                                                                                                                                                                                            07-JAN-1999; 99US-0115033P.
07-JAN-2000; 2000US-00479614.
                                                                                                                                                                                             07-APR-2003; 2003US-00409772.
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                                                                                                                                                                                                                                                                                                                                      Mccall C, Weber E;
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nes 16; Conserv
                                                                                                                                                                                                                                                                                   (MCCA/) MCCALL C.
                                                                                                                                                                                                                                                                                                   (WEBE/) WEBER E.
                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; ADG73236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 431 AA;
                                                                                                                          US2003216565-A1.
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                                                                                                                                                           20-NOV-2003
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to a novel monoclonal antibody (I) that specifically binds to a mammalian IgE epitope, where the epitope is between amino acids 145-166 or 356-374 of mammalian IgE, e.g. dog IgE.

(I) is useful for testing an allergen reactivity of an IgE sample. The allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut or corn allergens. The sample is a biological sample collected from a dog, cat or horse. (I) is also useful for detecting mammalian IgE and for treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal antibodies recognise epitopes on canine IgE corresponding to amino acid cesiques 357-371 (ADRIGG1) and 146-162 (ADRIGG09) respectively of the canine IgE epsilon-chain. Recognition of epsilon-chains from IgE from cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and 3.76 was companion of IgE from cat and horse, but did not exhibit cross-reactivity with the epsilon-chain of IgE from cat loss human epsilon-chains of IgE. The present sequence is the cat IgE 3.76 recognition site.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel antibody that specifically binds to mammalian IgE epitope, useful for testing an allergen reactivity of IgE sample, detecting mammalian IgE or treating asthma or anaphylactic shock.
                                                                                                                                                                                               Antiasthmatic; Antiallergic; Immunosuppressive; IgE; dog; asthma; anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                           Cat IgE epitope recognised by monoclonal antibody 3.76, SEQ ID 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
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                                                      ADR10610 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                              (UYNC-) UNIV NORTH CAROLINA STATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 6; Page 9; 14pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                             16-JAN-2003; 2003US-0440472P
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                                                                                                                                                                                                                                                                                                                                                                         15-JAN-2004; 2004WO-US003566
                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                     WO2004065936-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hammerberg B;
                                                                                                                            21-OCT-2004
                                                                                                                                                                                                                                                                  Felis catus.
                                                                                                                                                                                                                                                                                                                                        05-AUG-2004
                                                                                         ADR10610;
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Gaps

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Length 431; 0; Indels

89.7%; Score 87; DB 8; Le 100.0%; Pred. No. 8.7e-06; iive 0; Mismatches 0;

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Immunoglobulin B; vaccine; IgB; cytotoxic T lymphocyte response; immune response; major histocompatibility complex; MHC; immunogenic; antiallergic; antiasthmatic; immunosuppressive vasotropic; cytostatic; dermatological; antiinflammatory; IgB-mediated condition; food allergy; atopic hypersensitivity condition; allergic athma; atopic dermatitis; non-atopic hypersensitivity condition; anaphylaxis;
                                                                                    Cat IgE heavy chain amino acid sequence SEQ ID NO:25.
                                                                                                                                                                                                                                                                                                                            08-AUG-2002; 2002WO-US026986.
                                                        (first entry)
                                                                                                                                                                                                            urticaria hives
                                                                                                                                                                                                                                                                   WO2003015716-A2
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                                                                                                                                                                                                                                       Felis catus
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ADG73237 standard; protein; 431 AA.

RESULT 7 ADG73237 (first entry)

11-MAR-2004

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                                                                                                                                                                                                       The present invention describes a method (M1) for identifying peptides that induce cytotoxic T-lymphocyte (CTL) response against immunoglobulin EE [IgB], comprising providing a test peptide (T) suspected of being able to bind to major histocompatibility complex (MHC) class I molecule, and evaluating (T) for ability to elicit in a mammal a CTL response to induces such a response is identified. Also described are compositions: (CL) comprising at least one immunogenic peptide (I) identified by (MI); (C2) comprising at least one isolated polynucleotide encoding (I); and (C2) comprising at least one isolated polynucleotide encoding (I); and (C2) comprising at least one isolated polynucleotide are compositions: (C1) comprising at least one isolated polynucleotide and presented (C3) comprising at least one isolated polynucleotide encoding (I); and (C3) comprising at least one isolated polynucleotide and presented (C3) comprising at least one isolated polynucleotide and presented (C3) comprising at least one isolated polynucleotide and presented (C3) comprising at least on a least one used as inducers of a CTL response against IgE, and in can be used as inducers of a CTL response against IgE, and in vaccines. C1-3 can be used for modulating an IgE-mediated condition in a mammal. C1-3 are useful for modulating an IgE-mediated condition in a completed atopic hypersensitivity condition, IgE mediated on altergic rhinitis, allergic asthma, food allergies, or atopic dermatitis), non-atopic hypersensitivity conditions (such as anaphylaxis, and urticaria thirds). The present sequence represents an IgE heavy chain amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                               Identifying peptides that induce cytotoxic T-lymphocyte, CTL response against IgB, by identifying peptide eliciting CTL response to IgE peptides naturally presented by major histocompatibility complex class I protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Feline, immunoglobulin E; IgE epsilon heavy chain, parasitic infection, IgE-mediated immune response, allergy; neoplasia, vaccine technology; antibody technology, antiallergic, antiparasitic, cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hives). The present sequence represents an IgE heavy chain amino acid sequence, which is given in an example from the present invention
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                                                        Chen Z;
                                                                                                                                                                                 Example 7; Page 145-147; 187pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABU09338 standard; protein; 496 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Feline IgE epsilon heavy chain #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.08; PLU
                                                       Chen SA, Yang Y, Barankiewicz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                216 VDGQKATNIFPYTAPG 231
13-AUG-2001; 2001US-031Z120P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-JAN-2000; 2000US-00479614.
                          (IGET-) IGE THERAPEUTICS INC.
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nes 16; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABU09338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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The present invention relates to the isolation of feline immunoglobulin E (IgE) kappa light chain and tgg epsilon heavy chain proteins, and the polynucleotide sequences encoding them. The sequences of the invention are useful for treating feline IgE-mediated immune responses (e.g. allergies, parasitic infections or neoplasia), in vaccine technology, small molecule/antibody technology, molecular biology, and various immunological techniques related to feline IgE and its functions. The present sequence represents feline IgE epsilon heavy chain #2
                                                                                                                                                                                                                                      New nucleic acid molecule encoding feline immunoglobulin E (IgE) heavy or light chain protein, useful for treating feline IgE-mediated responses e.g. allergies, parasitic infections or neoplasia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Feline, immunoglobulin E; IgE epsilon heavy chain, parasitic infection, IgE-mediated immune response, allergy, neoplasia, vaccine technology; antibody technology, antiallergic, antiparasitic, cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID No:8 and is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "This sequence is given as SEQ ID No:14 and specifically claimed in Claim 12" 284. 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence is given as SEQ ID No:11 and claimed in Claim 9"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89.7%; Score 87; DB 6; Length 496; 100.0%; Pred. No. 1e-05; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 37-39; 45pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Feline IgE epsilon heavy chain #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "This
specifically
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99US-0115033P
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                                                                                                                                                                       WPI; 2003-391997/37.
N-PSDB; ABX95715.
                                                                                                                       Mccall C, Weber E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
ses 16; Conserv
                                             (MCCA/) MCCALL C. (WEBE/) WEBER E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 496 AA;
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07-JAN-1999;
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                                                                                                                                                                                                                                                                                                The present invention relates to the isolation of feline immunoglobulin I (IgB) kappa light chain and IgE epsilon heavy chain proteins, and the polynuclectide sequences encoding them. The sequences of the invention are useful for treating feline IgE-mediated immune responses (e.g. allergies, parasitic infections or neoplasia), in vaccine technology, amall molecule/antibody technology, molecular biology, and various immunological techniques related to feline IgE and its functions. The present sequence represents feline IgE epsilon heavy chain #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated nucleic acid molecule encoding a portion of a feline IgE heavy chain protein, useful for treating and/or eliciting feline immune responses for IGE-mediated responses, such as allergies.
                                                                                                                                                                              New nucleic acid molecule encoding feline immunoglobulin E (IgE) heavy light chain protein, useful for treating feline IgE-mediated responses e.g. allergies, parasitic infections or neoplasia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antiallergic, IgE-modulator, vaccine, feline, IgE, immunoglobulin E, immune response, IgE-mediated response, allergy, cat, heavy chain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cat partial immunoglobulin E (IgE) heavy chain #2.
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100.0%; Pre
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                                                                                Weber E;
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N-PSDB; ADG73250.
                     (MCCA/) MCCALL C. (WEBE/) WEBER E.
                                                                                                                                             N-PSDB; ABX95713.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 496 AA;
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The invention describes an isolated nucleic acid molecule (I) encoding a portion of a feline IgE heavy chain protein. The methods and compositions of the present invention are useful for eliciting feline immune responses for and/or treating IGE-mediated responses, such as allergies. This is the amino acid sequence of a partial cat immunoglobulin E (IgE) heavy
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100.0%; Pred. No. 1e-05;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                    89.7%; Score 87; DB 8; 100.0%; Pred. No. 1e-05;
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|||||| |:|||||| 295 VDGQKAENLFPYTAP 309 1 VDGQKATNIFPYTAP 15

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naturally processed and presented light peptides, where a peptide that induces such a response is identified. Also described are compositions: (C1) comprising at least one immunogenic peptide (I) identified by (M1); (C2) comprising at least one isolated polynucleotide encoding (I); and (C3) comprising antigen-presenting cells that recognise at least one (I). Where C1-3 are able to bind to at least one MHC class I molecule and to elicit in a mammal a CTL response to naturally processed and presented IGE peptides. C1-3 have antiallergic, antiasthmatic, immunosuppressive, vasotropic, dermatological, antiinflammatory and cytostataic activities, and can be used as inducers of a CTL response against IgE, and in vaccines. C1-3 can be used for modulating an IgE-mediated condition in a mammal. C1. C1-3 are useful for modulating an IgE-mediated condition in a ligh-mediated atopic hypersensitivity condition, IgE myeloma in a mammal. Preferably, C1-3 are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        useful for treating atopic hypersensitivity conditions (such as allergic rhinitis, allergic asthma, food allergies, or atopic dermatitis), non-atopic hypersensitivity conditions (such as anaphylaxis, and urticaria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 that induce cytotoxic T-lymphocyte (CTL) response against immunoglobulin B (IgB), comprising providing a test peptide (T) suspected of being able to bind to major histocompatibility complex (WHC) class I molecule, and evaluating (T) for ability to elicit in a mammal a CTL response to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antiallergic; antiachmatic; immunosuppressive; vasotropic; cytostatic; dermatological; antiinflammatory; IgE-mediated condition; food allergy; atopic hypersensitivity condition; allergic rhinitis; allergic asthma; atopic dermatitis; non-atopic hypersensitivity condition; anaphylaxis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying peptides that induce cytotoxic T-lymphocyte, CTL response against IgE, by identifying peptide eliciting CTL response to IgE peptides naturally presented by major histocompatibility complex class
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        present invention describes a method (M1) for identifying peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hives). The present sequence represents an IgE heavy chain amino acid sequence, which is given in an example from the present invention
                                                                                                                                                                                                                                                                                                       Duckbilled platypus IgE heavy chain amino acid sequence SEQ ID NO:29
                                                                                                                                                                                                                                                                                                                                                                                                                                            immunogenic;
                                                                                                                                                                                                                                                                                                                                                                                          Immunoglobulin E; vaccine; IgE; cytotoxic T lymphocyte response; immune response; major histocompatibility complex; MHC; immunoger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chen Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 7; Page 154-157; 187pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen SA, Yang Y, Barankiewicz T,
                                              ABP96584 standard; protein; 577 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-AUG-2002; 2002WO-US026986.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-AUG-2001; 2001US-0312120P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (IGET-) IGE THERAPEUTICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 86.,.,
Asa 13; Conservative
                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ornithorhynchus anatinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-268242/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 577 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     urticaria hives.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO2003015716-A2.
                                                                                                                                                                                                                    28-MAY-2003
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                                                                                                                            ABP96584;
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ABP96584
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                                                                                                                                  Platypus; immunoglobulin B; IgE; vaccination; infection; allergy; asthma; eczema; immunogenic peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is an immunogenic peptide consisting of the heavy chain constant regions 2, 3 and 4 of the platypus IGE. It was used to construct a number of immunogenic peptides which consisted of regions of IGE from different mammals, which appear to cause a stronger polyclonal anti-self IGE response than peptides consisting of the same regions from one mammal. Immunogenic peptides, particularly those consisting of different heavy chain constant regions, can be used for vaccination in humans, against bacterial and viral infections and allergies, such as asthma, fur, pollen and food allergies and eczema
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunogenic polypeptides useful for preventing the harmful effects of immunoglobulin \boldsymbol{E} in mammals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                        Platypus IgE heavy chain constant regions 2, 3 and 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                              /note= "Xaa=unknown"
                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADF90022 standard; protein; 337 AA.
                        AAB06204 standard; protein; 343 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure, Fig 2; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7
                                                                                                                                                                                                                       1. .343
/label= OTHER
                                                                                                                                                                                                                                                                                                                                                          98US-0106652P.
99US-00401636.
                                                                                                                                                                                                                                                                                                                                  99WO-SE001896.
                                                                                                                                                                                                                                                                                                                                                                                                      (RESI-) RESISTENTIA PHARM AB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 VDGQKATNIFPYTAP 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ||||||| ::||||||
61 VDGQKAEHLFPYTAP 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                            22-NOV-2000 (first entry)
                                                                                                                                                                           Ornithorhynchus anatinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-365342/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
es 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 343 AA;
                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                           WO200025722-A2
                                                                                                                                                                                                                                                                                                                                21-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                            02-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                          22-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-FEB-2004
                                                                                                                                                                                                                                                                                                     11-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                              Hellman LT;
                                                    AAB06204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADF90022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADF90022
RESULT
                                        SXXXE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
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Gaps

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Score 73; DB 6; Length 577; Pred. No. 0.0026; 1; Mismatches 1; Indels

75.3%; 86.7%;

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The present sequence is the protein sequence of an opossum CH2-rat CH3-opossum CH4 (ORO) chimeric IgE polypeptide. A vector comprising a nucleic acid encoding ORO can be used for recombinant production of this chimeric IgE in host, e.g. CHO, cells. The invention provides methods and materials related to expressing chimeric IgE proteins. Nucleic acid vectors, host cells, and methods for producing chimeric IgE polypeptides are provided. When administered to a mammal, the chimeric polypeptides can reduce the IgE antibody effects of IgE-related diseases such as asthma, allergies and eczema.
                                                                                                                                                                                                                                                                                                                                                                                                                New host cell comprising a nucleic acid vector comprising a cytomegalovirus promoter, an Ig leader sequence, an insert sequence or SV40 late polyadenylation sequence, useful in producing a chimeric IgE polypeptide.
                                        IgB; immunoglobulin; antibody; opossum; rat; vaccine; antiallergic; antiasthmatic; dermatological.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59.8%; Score 58; DB 8; Length 337; 76.9%; Pred. No. 0.48; ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                      Lundgren M, Fuentes A, Magnusson A;
              Opossum-rat chimeric IgE polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 3; SEQ ID NO 3; 23pp; English.
                                                                                                                                                                                                                                   15-MAY-2003; 2003WO-IB002503.
                                                                                                                                                                                                                                                                                                      (RESI-) RESISTENTIA PHARM AB.
                                                                                                                                                                                                                                                                      21-MAY-2002; 2002US-0382552P
                                                                                                                                                                                                                                                                                                                                                                         WPI; 2004-042496/04.
N-PSDB; ADF90020, ADF90021.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 76.9
Matches 10; Conservative
                                                                                               Chimeric.
Didelphis virginiana.
Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 337 AA;
                                                                                                                                                                   WO2003096966-A2
                                                                                                                                                                                                   27-NOV-2003.
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Search completed: August 30, 2006, 04:22:02 Job time : 65.4545 secs ||||:| |:||| 56 VDGQEAENLFPYT 68 q

1 VDGQKATNIFPYT 13

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Gaps

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Page

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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- protein search, using sw model	August 30, 2006, 04:29:42 ; Search time 10.7273
OM protein	Run on:

August 30, 2006, 04:29:42; Search time 10.7273 Seconds (without alignments) 161.448 Million cell updates/sec

US-10-758-165A-9 97

1 VDGQKATNIFPYTAPGTK 18 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		d				SUMMARIES	
Result No.	Score	Query Match	/ n Length		DB	ID .	Description
	48	49.	5 27	270		T16880	hypothetical prote
7	46	47.4		579	N	JW0071	asparagine synthas
m	46	47.4	4 58	96	7	S69183	
4	46	47.4	4 65	8	N	AH0110	probable surface p
S	45	46.4		0	7	G95009	sensor histidine k
9	45	46.4		.0	7	E97881	histidine kinase (
7	45	46.4	58	583	_	AJ PMN2	asparagine synthas
80	44	45.4	51	=	7	T16279	hypothetical prote
6	43	44	32	2	~	AD3488	transporter BMEI18
10	43	44.	3 28	98	Н	AJPMN1	asparagine synthas
11	42	43.3		86	2	AF0306	puative trans-acon
12	42	43.	38	31	ď	AD2436	ATP-binding protei
13	42	43.3		476	7	AC2465	6-phosphogluconate
14	42	43.3		33	a	T22177	hypothetical prote
15	42	43.3		33	7	B71325	conserved hypothet
16	42	43.3	7	98	7	A87692	conserved hypothet
17	41	42.3		=	7	T17798	hypothetical prote
18	41	42.3		272	7	H87075	probable conserved
19	41	42.3		6.5	7	C83039	probable permease
20	41	42.3		2	~	JC5722	vacuolar protein s
21	41	42.3		619	N	H84416	hypothetical prote
22	41	42.	3 64:	23	_	S15623	
23	41	42.	7	13	0	JE0230	NADPH-cytochrome P
24	41	42.3	3 85	6.0	~	AE2217	hypothetical prote
25	41	42.3		606	a	T06246	aspartate kinase (
56	41	42.3		916	~	T06242	aspartate kinase (
27	41	42.3	_	22	7	S74487	hypothetical prote
28	41	42	_	.055.	~	C82600	44
59	40.5	41.	9 75	92	0	B83608	hypothetical prote

conserved hypothet	hypothetical prote	hypothetical prote	conserved hypothet	asparagine synthas	gene 59 protein -	conserved hypothet	serine proteinase	probable membrane	hypothetical prote	protein-glutamate	probable polyamine	spermidine/putresc	conserved hypothet	BH0982 hypothetica	asparagine synthas
G69203	F89886	A83751	D90167	549846	GMBPT4	C75582	C89967	T03109	S40753	A48511	G81926	C81179	AH2821	H97599	T12989
0	0	7	~	7	٦	7	~	~	~	-	7	7	~	~	7
101	109	137	179	189	217	227	240	302	327	357	374	419	454	470	584
41.2	41.2	41.2	41.2	41.2	41.2	41.2	41.2	41.2	41.2	41.2	41.2	41.2	41.2	41.2	41.2
40	40	40	40	40	40	40	40	40	40	40	40	40	40	40	40
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

 RESULT 1 T16880
hypothetical protein T14G12.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence revision 20-Sep-1999 #text_change 05-Oct-2004
C;Accession: T16880
R;Wilcox, L.
submitted to the EMBL Data Library, November 1995
A; Description: The sequence of C. elegans cosmid T14G12.
A; Reference number: Z18596
A;Accession: T16880
A;Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A;Residues: 1-270 <wil></wil>
A; Cross-references: UNIPROT: Q22510; UNIPARC: UPI00000075025; EMBL: U41268; NID: 91086843; PI
C;Genetics:
A,Gene: CESP:T14G12.4
A;Introns: 37/1; 72/3; 164/1
F;93-185/Domain: fork head DNA-binding domain homology <fhd></fhd>

Gaps ö, Length 270; ; DB 2; 2; Mismatches 49.5%; Score 48; 57.1%; Pred. No. 3 Conservative Query Match Best Local Similarity

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205 GAAAANLFPYFSPG 218 3 GOKATNIFPYTAPG 16 ద ઠે

asparagine synthase (glutamine-hydrolysing) (EC 6.3.5.4) - soybean C;Species: Glycine max (soybean) C;Date: 13-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 09-Jul-2004

C;Accession: JW0071
R;Yamagata, H.; Nakajima, A.; Bowler, C.; Iwasaki, T.
Bisci. Biotechnol. Biochem. 62, 148-150, 1998
A;Title: Molecular cloning and characterization of a cDNA encoding asparagine synthetase A;Reference number: JW0071; MUID:98162148; PMID:9501527

A; Accession: JW0071

A; Molecule type: mRNA A; Residues: 1-579 < YAM>

A;Cross-references: UNIPROT:Q42792; UNIPARC:UPI00000A95EC; GB:U55874; NID:g1305548; PIDN C;Superfamily: asparagine synthase (glutamine-hydrolyzing)
C;Keywords: asparagine biosynthase
F;2-579/Product: asparagine synthase (glutamine-hydrolyzing) #status predicted <DUM>F;2/Active site: Cys #status predicted

Gaps 14; Length 579; 5; Indels Query Match
47.4%; Score 46; DB 2;
Best Local Similarity 34.4%; Pred. No. 10;
Matches 11; Conservative 2; Mismatches

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Gaps

.. 0

Length 350; Indels

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C;Species: Streptococcus pneumoniae
C;Species: Streptococcus pneumoniae
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C;Accession: E97891
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; E. e., R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M.; P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.; A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Attle: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Accession: E97881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Cross-references: UNIPROT:P19252; UNIPARC:UPI000016DF0B; EMBL:X52180; NID:G20651; PIDN C,Genetics:
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt, I.E. Science 293, 498-506, 2001
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Authors: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae. A;Reference number: A95000; MUD:21357209; PMID:11463916
A;Accession: G95009
A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPROT:Q9S1J1; UNIPROT:Q8DRKO; UNIPARC:UPI0000051BF0; GB:AE005672; A;Experimental source: strain TIGR4 C;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: C;Genetics: A;Genetics: A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPROT:Q9S1J1; UNIPROT:Q8DRK0; UNIPARC:UPI0000051BF0; GB:AE007317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (EC 6.3.5.4) [similarity] - garden pea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 histidine kinase (EC 2.7.3.-) [imported] - Streptococcus pneumoniae (strain R6)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             asparagine synthase (glutamine-hydrolysing) (EC 6.3.5.4) [similarity] - gard asparagine synthetase (glutamine-hydrolyzing) - gard Cipecies: Pisum sativum (garden pea) (c)baccies: Disum sativum (garden pea) (c)baccesion: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004 (c)baccesion: S11443 (G.M. EMBO J. 9, 323-332, 1990 (A.M. EMBO J. 9, 323-332, 1990 (
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C;Superfamily: asparagine synthase (glutamine-hydrolyzing)
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Pred. No. 8.6;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ed. No. 8.6;
Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 46.4
Best Local Similarity 72.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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| NAFKYSAPGTK 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         248 NAFKYSAPGTK 258
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A;Residues: 1-583 <TSA>
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A;Molecule type: DNA
A;Residues: 1-350 <KUR>
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C;Species: Streptococcus pneumoniae
C;Species: Streptococcus pneumoniae
C;Actesion: G3-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C;Accession: G95009
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable surface protein (partial) YP00902 [imported] - Versinia pestis (strain C092) C;Species: Yersinia pestis (c;Species: Yersinia pestis (c;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004 C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004 R;Parkhill, J; Wren, B40110 R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Nature 413, 523-527, 2:001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague. A;Reference number: AB0001; MUID:21470413; PMID:11586360 A;Gression: AH0110 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-658 <KUR>
A;Residues: 1-658 <KUR>
A;Conetics: C;Genetics: UNIPROT:QBZHJO; UNIPARC:UPI0000CD765; GB:AL590842; PIDN:CAC89747.1;
                                                                                                                                                                                                                                                                                                                                                                                                                           asparagine synthase (glutamine-hydrolysing) (EC 6.3.5.4) - Lotus japonicus C;Species: Lotus japonicus c;Species: Lotus japonicus c;Species: Lotus japonicus c;Species: Lotus japonicus c;Space: Lotus separagine;Space: Lotus c;Space: Lotus
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A;Cross-references: UNIPROT:P49093; UNIPARC:UPI000016DE2B; EMBL:X89410; NID:g897772;
A;Experimental source: strain B-129
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A Gene: AS2
C; Superfamily: asparagine synthase (glutamine-hydrolyzing)
C; Keywords: asparagine biosynthesis; ligase
F;2-586/Product: asparagine synthase (glutamine-hydrolyzing) #status predicted <DUM>F;2/Active site: Cys #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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Pred. No. 10;
4; Mismatches
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Best Local Similarity 52.9%;
Matches 9; Conservative
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Best Local Similarity 31.2
Matches 10; Conservative
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A, Residues: 1-586 <TSA>
A, Cross-references: UNIPROT.P19251; UNIPARC:UDF00016DF0A; EMBL:X52179; NID:g20649; PIDN A; Cross-references: UNIPROT.P19251; UNIPARC:UDF00016DF0A; EMBL:X52179; NID:g20649; PIDN C; Common: This protein is one of a family of glucamine aminator domain, and a glutamine am an aminator domain, which catalyzes the ammonia-dependent reaction, and a glutamine am
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Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
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**Razkhili, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davies, P.; Dougan, G.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Mature 413, 523-527, 2001

**Affitle: Genome sequence of Yersinia pestis, the causative agent of plague.

**Affitle: Genome sequence of Wersinia pestis, PMID:11586360
                                                                                                                                                                                                                                                                                                                      C,Accession: S11444

R,Tsai, F.Y.; Coruzzi, G.M.

R,BMD J. 9, 3123-132, 1999

A,Title: Dark-induced and organ-specific expression of two asparagine synthetase genes
A,Reference number: S11443; MUID:90151604; PMID:1968003
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F;2-586/Product: asparagine synthase (glutamine-hydrolyzing) #status predicted <MAT>
F;175-586/Domain: aminator <AMN>
                                                                      - garden pea
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A;Note: Nostec sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 31-Dec-2004
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C.Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
                                                        asparagine synthase (glutamine-hydrolysing) (EC 6.3.5.4) [similarity] - gar NiAlternate names: asparagine synthetase (glutamine-hydrolyzing) (C.Species: Pisum sativum (garden paragent) (C.Species: Pisum sativum (garden pervision 31-Dec-1991 #sequence_revision 31-Dec-1991 #sequen
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C;Superfamily: bioC protein; bioC homology
C;Keywords: methyltransferase
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Matches 7; Conservative
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482 ASHIFPFNTPNTK 494
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A,Molecule type: DNA
A,Residues: 1-258 <KUR>
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A; Molecule type: DNA
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R;DelVeccohio, V. O.; Kapatral, V., Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, S;DelVecchio, V. O.; Kapatral, V. Selkov, E.; Selkov, E.; Selkov, E.; Selkov, E.; Selkov, E.; P. Selkov, E
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-322 <KUR>
A;Cross-references: UNIPROT:Q8YEI8; UNIPARC:UPI0000058245; GB:AE008917; PIDN:AAL53071.1;
A;Experimental source: strain 16M
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C;Keywords: asparagine biosynthesis; ligase
F;2-583/Product: asparagine synthase (glutamine-hydrolyzing) #status predicted <MAT>
F;2/Active site: Cys #status predicted
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Cibate: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
Cibate: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
Cibate: 218-20-Sep-1999 #sequence of Cibate Sample Sam
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C;Date: 01-Feb_2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
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C;Superfamily: Caenorhabditis elegans hypothetical protein F35H10.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 45.4%; Score 44; DB 2; Length 511; Best Local Similarity 43.8%; Pred. No. 19; Matches 7; Conservative 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44.3%; Score 43; DB 2; Length 322;
47.1%; Pred. No. 17;
tive 3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                    Score 45; DB 1; Length 583;
Pred. No. 15;
2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein F35H10.7 - Caenorhabditis elegans
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GOKATNIFPYTAPGTK 18 |:| :|:|: GEKIVSIYPHRKPATK 41

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A, Gene: CESP: F35H10.7

C,Genetics:

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RESULT 10

Local Similarity 47.1 nes 8; Conservative

Best Loc Matches

A; Map position: I C;Genetics: A;Gene: BMEI1890

Query Match

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Best Local Similarity 50.0%; Pred. No. 53; Matches 11; Conservative 1; Mismatches
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6-phosphogluconate dehydrogenase [imported] - Nostoc sp. (strain PCC 7120)

C; Species: Nostoc sp. PCC 7120

A;Note: Nostoc sp. PCC 7120

C; Decles: Nostoc sp. PCC 7120

C; Decles: Nostoc sp. Strain PCC 7120

A; Raneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazawai, N.; Yamada, M.; Yasuda, M.; Tabata, Sp. Nakazence number: Assumer of the Filamentous Nitrogen-fixing Cyanobacterium Ana A; Reserience number: Assumer Sp. MulD:21595285; PMID:11759840

A; Status: preliminary

A; Status: preliminary

A; Status: Decliminary

A; Ressidues: 1-476 cKIRs

A; Cross-references: UNIPROT:Q8YLM3; UNIPARC:UPI0000CEE0D; GB:BA000019; PIDN:BAB76974.1;
A; Experimental source: strain PCC 7120

C; Genetics:
A; A; Genetics:
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T22177

hypothetical protein F44F1.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T22177
R;Dobson, R.
Submitted to the EMBL Data Library, October 1996
A;Recession: T22177
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Accession: T22177
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-63 a/WIL>
A;Accession: 1-63 a/WIL>
A;Accession: C;Genetics: 1-63 a/WIL>
A;Accession: 1-63
     DNA Res. 8, 205-213, 2001

Aritle: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana Aritle: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A; Reference number: AB1807; MUID:21595285; PMID:11759840

A; Accession: AD2436

A; Status: preliminary

A; Status: preliminary

A; Molecule type: DNA

A; Residues: 1-381 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:Q8YM92; UNIPARC:UPI0000CED3F; GB:BA000019; PIDN:BAB76743.1;
A;Experimental source: strain PCC 7120
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43.3%; Score 42; DB 2; Length 476;
Best Local Similarity 72.7%; Pred. No. 39;
Matches 8; Conservative 0; Mismatches 3; Indel8
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A;Introns: 43/2; 69/3; 181/3; 241/2; 493/3; 526/2; 548/3
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31;
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Pred. No.
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Best Local Similarity 53.3
Matches 8; Conservative
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A, Gene: all5044
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C,Accession: B71325
R,Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin: Seno, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDo: they, L.; Weidman, J.; Snith, H.O.; Venter, J.G.
Science 281, 375-388, 1998
A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A;Reference number: A71226; MUID:98332770; PMID:966876
A;Accession: B71325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-683 <COL>A;Residues: 1-683 <COL>A;Cross-references: UNIPROT:083436; UNIPARC:UPI00000C0A71; GB:AE001220; GB:AE000520; NIDA;Experimental source: strain Nichols
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                                                                                                                                                                                                                                                                          conserved hypothetical protein TP0421 - syphilis spirochete
C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Date: 24-Jul_1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
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Indels
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50.0%; Pred. No. 59;
tive 3; Mismatches
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                                                                                                                      152 VDGÓWKTIIIDDYFPÝTTDGIR 173
                                                            1 VDGQKATNI----FPYTAPGTK 18
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Best Local Similarity 50.08
Matches 7; Conservative
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Q7P5V1_FUSNV
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07P5V1 FUSNV
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ID Q7
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022510 caenorhabdi
036vf1 rhodopseudo
0608x6 methylococc
094h26 oryza sativ
094h26 oryza sativ
095ga9 glycine max
042792 glycine max
095m55 phaseolus v
095m55 phaseolus v
095m57 phaseolus v
095m57 phaseolus v
095km1 yersinia pe
0212w7 bordetella
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0619h6 caenorhabdi
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237.245 Million cell updates/sec
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                                                                                      Seconds
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Q9aya0
Q9zhq4
Q3ma44
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                                                                                     August 30, 2006, 04:22:32 ; Search time 70.1818
GenCore version 5.1.9 (c) 1993 - 2006 Biocceleration Ltd
                                                                                                                                                                                                                                                                                   2849598
                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                    2849598 segs, 925015592 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   094426 ORYSA
097VU1 CHLRE
P93168 SOYBN
0381A6 SOYBN
042792 SOYBN
098M55 PHAVU
ASNS2 LOTJA
08CKM1 YERPE
08CKM1 YERPE
02LU7W7 BORAV
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Q619H6_CAEBR
Q8DRKO_STRR6
Q9SLJ1_STRPN
ALN_STRCO
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Q8R6B3_FUSNN
Q95QA9_CAEEL
Q22510_CAEEL
Q36VF1_RHOPA
Q608X6_METCA
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Q3VAY9 9SPHN
Q9AYA0 ORYSA
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Q3MA44_ANAVT
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QBRVL0 9FABA
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                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                       OM protein - protein search, using sw model
                                                                                                                                                                                                       BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                           1 VDGQKATNIFPYTAPGTK 18
                                                                                                                                                                                                                                                                                                                                                                                                                   UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*
                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Match Length DB
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                         astragalus
                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=C71;
US DOB Joint Genome Institute (JGI-PGF);
Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T., Hammon N., Israni S., Pitluck S., Richardson P.;
"Sequencing of the draft genome and assembly of Nitrosomonas eutropha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=C71;
US DOB Joint Genome Institute (JGI-ORNL);
Larimer F., Land M., Hauser L.;
"Annotation of the draft genome assembly of Nitrosomonas eutropha
                                                                                                                                                                                                                                                                                                                                                         Nitrosomonas eutropha C71.
Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
Nitrosomonadaceae; Nitrosomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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Q20069
Q6all1
Q9ab61
Q84x69
Q853q04
Q6lv7
Q6lv7
Q7alg
Q53jx1
Q2zh01
Q7xsp1
Q7xxp2
Q7xxp2
Q7xxp2
Q7xxp2
Q7xxp2
                                                                                                                                                                                                                                                                                         25-0cT-2005, integrated into UniprotKB/TrEMBL..
25-0CT-2005, sequence version 1.
27-PEB-2006, entry version 3.
Putative type 4 finbrial biogenesis protein PilY1 precursor.
ORFNames=NeutDRAFT_0559;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1143;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29 Potential.
123766 MW; 9C270A88F6A0FAF1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C71.";
Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54.6%; Score 53; DB 2;
62.5%; Pred. No. 16;
cive 1; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AAJE01000019; EA016686.1; -; Genomic_DNA
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                                                                                                           Q2ZH01_CALSA
Q7FAL2_ORYSA
Q7XSP1_ORYSA
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                                                                                      ORYSA
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                                                              PROMT
                                                                                                                                                   Q70XV6 AMBTC
Q2R0G5 ORYSA
                                              Q53Q04 ORYSA
                                                                           ORYSA
U171_CAE
Q6ALL1_D
Q9MB61_A
Q84X69_9
                                                           Q46LV7_F
Q6UUM4_C
Q7FA19_C
Q53JX1_C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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Best Local Similarity 62.5
Matches 10; Conservative
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NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=335283;
Q3N7VI 9PROT ID Q3N7VI 9PROT
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Length 382;

43923 MW; 93038D4296AE34CD CRC64;

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InterPro; IPR010327; HGD-D.
Pfam; PF06050; HGD-D; 1.
                                              Complete proteome; Lyase. SEQUENCE 382 AA; 43923
                                                                                                                   Query Match
Best Local Similarity
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Q95QA9;
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Q95QA9_CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                     STRAIN-ATCC 49256;

Karpatral V., Ivanova N., Anderson I., Reznik G., Bhattacharyya A., Gardner W.L., Mikhailova N., Larsen N., D'Souza M., Walunas T., Haselkorn R., Overbeek R., Kyrpides N.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=ATCC 25586;
MEDLINE=21886394; PubMed=11889109;
DOI=10.1128/JB.184.7.2005-2018.2002;
Kapatral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A Bhattacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L., Vasieva O., Chu L., Kogan Y., Chaga O., Goltsman E., Bernal A., Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R., Fonstein M., Kyrpides N.C., Overbeek R.;
"Genome sequence and analysis of the oral bacterium Fusobacterium nucleatum strain ATCC 25586.";
                        15-DEC-2003, integrated into UniProtKB/TrEMBL.
15-DEC-2003, sequence version 1.
07-FBB-2006, entry version 8.
(R)-2-hydroxyglutaryl-CoA dehydratase beta-subunit (EC 4.2.1.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (R)-2-hydroxyglutaryl-CoA dehydratase beta-subunit (EC 4.2.1.-). OrderedLocusNames=FN0208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52.6%; Score 51; DB 2; Length 382; 64.3%; Pred. No. 11; 3; Indels ive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fusobacterium nucleatum subsp. nucleatum.
Bacteria; Fusobacteria; Fusobacterales; Fusobacteriaceae;
                                                                                                                                              Fusobacterium nucleatum subsp. vincentii ATCC 49256.
Bacteria; Fusobacteria; Fusobacterales; Fusobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               382 AA; 43893 MW; 441C73816E1C761E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, AABF01000055; EAA24105.1; -; Genomic_DNA.
GO; GO:0016829; F:lyase activity; IEA.
InterPro; IPR010327; HGD-D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2002, integrated into UniProtKB/TrEMBL 01-JUN-2002, sequence version 1. 07-FEB-2006, entry version 16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           382 AA
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BioCyc, FNUC190304:FN0208-MONOMER; -.
GO; GO:0016829; F:lyase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QBR6B3_FUSNN PRELIMINARY; PRT;
QBR6B3;
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28 EGKKAVGIFPYYAP 41
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Best Local Similarity 64...
Best Local 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             preliminary data.
                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                               Fusobacterium.
NCBI_TaxID=209882;
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                                                                                                                          Name=FNV1343;
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R Bnsembl; T14G12-4; Caenorhabditis elegans.

R WormBase; WBGENE00001434; Ikh-2.

R WormBase; Wachene00001434; Ikh-2.

R WormBase; Wachene00001434; Ikh-2.

R GO; GO:0005634; C:nucleus; IEA.

R GO; GO:0006359; P:regulation of transcription, DNA-dependent; IEA.

R GO; GO:0006359; P:regulation of transcription, DNA-dependent; IEA.

R GO; GO:0006359; P:regulation of transcription, DNA-dependent; IEA.

R InterPro; IPRO11991; Wing hlx_DNA_bd.

R PRINTS; PRO0250; Fork head; 1.

R PRINTS; PRO0250; FORKHEAD.

R PRODOM; PD000425; FF Fork head; 1.

SMART; SMO0339; FH; I.
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                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916; DOI=10.1126/science.282.5396.2012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00658; FORK_HEAD_2; 1.
PROSITE; PS50039; FORK_HEAD_3; 1.
Complete protecome; DNA-binding; Nuclear protein; Transcription;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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"Genome sequence of the nematode C. elegans: a platform for investigating biology.";
Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 168;
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                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                     07-FEB-2006, entry version 28.
Forkhead transcription factor family protein 2, isoform Name=fkh-2; ORFNames=T14G12.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transcription regulation.
SEQUENCE 168 AA; 19239 MW; 8E01AC4E69968572 CRC64;
Score 51; DB 2;
Pred. No. 11;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49.5%; Score 48; DB 2; 57.1%; Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                           01-DEC-2001, integrated into UniProtKB/TrEMBL 01-DEC-2001, sequence version 1.
                                                                                                                                                                                                                                                                                                  168 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U41268; AAL02521.1; -; Genomic_DNA.
HSSP; Q99988; IDSV.
                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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     52.6%;
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103 GAAAANLFPYFSPG 116
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                                                                                                             2 DGQKATNIFPYTAP 15
                                                                                                                                                               28 EĞKKAVGİFPYYAP 41
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                                                            9; Conservative
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Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=6239;
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Q22510 CAEEL
ID Q22510_CAEEL
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DOE Joint Genome Institute (JGI-PGF);
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=414;
                                                                                                                                                                                            STRAIN=BisA53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OG08X6 METCA
                                                                                                                                                                                                                                                                                                                    Submitted
                                                                                                                                                                                                                                                                                             BisA53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q608X6_METCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q608X6;
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                                                                                                                                                              Bukaryota; Metazoa; Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                        STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916; DOI=10.1126/science.282.5396.2012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00657; FORK HEAD 1; 1.
PROSITE; PS00658; FORK HEAD 2; 1.
PROSITE; PS50039; FORK HEAD 3; 1.
Complete proteome; DNA-binding; Nuclear protein; Transcription;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9XW88 php-3; NbExp=1; Intact=EBI-327741, EBI-316766; Q21648:R02F2.5; NbExp=1; Intact=EBI-327741, EBI-314179; SUBCELDULAR LOCATION: Nuclear (By similarity).
                                                                                                                                                                                                                                                                                                                                         The C. elegans sequencing consortium; "Genome sequence of the nematode C. elegans: a platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Rhodopseudomonas.
                                             01-NOV-1996, sequence version 1.
7-FRB-2006, entry version 39.
Forkhead transcription factor family protein 2, isoform a.
Name=fkh-2; ORFNames=T14G12.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49.5%; Score 48; DB 2; Length 270;
57.1%; Pred. No. 24;
tive 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         270 AA; 30491 MW; 7C49116E5EC76175 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q36VF1 RHOPA PRELIMINARY; PRT; 365 AA. Q36VR1; 06-DBC-2005, integrated into UniProtKB/TrEMBL.
                         01-NOV-1996, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP, Q99958; 1D5V.

SMR; Q22510; 93-170.

IntAct; Q22510; --

Ensembl; T14G12.4; Caenorhabditis elegans.

WormBep; T14G12.4; CE04965.

GO; GO:0005515; F:protein binding; IPI.

InterPro; IPR011991; Wing_hlx_DNA_bd.

Pfam; PF00250; Fork head; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U41268; AAA82436.1; -; Genomic_DNA.
PIR; T16880; T16880.
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ProDom; PD000425; TF Fork head; 1.
SMART; SM00339; FH; 1.
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Rhodopseudomonas palustris BisA53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-DEC-2005, sequence version 1.
07-FEB-2006, entry version 3.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                       investigating biology.";
Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAAAANLFPYFSPG 218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 57.1 tes 8; Conservative
                                                                                                                                       Caenorhabditis elegans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- INTERACTION:
                                                                                                                                                                                                                   NCBI_TaxID=6239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-Bath / NCIMB 1113;
PubMed=15383840; DOI=10.1371/journal.pbio.0020303;
PubMed=15383840; DOI=10.1371/journal.pbio.0020303;
PubMed=15383840; DOI=10.1371/journal.pbio.0020303;
Parsen O., Sakwa U., Bruseth L., Khouri H.M., Durkin A.S., Dimitrov G., Jiang L., Scanlan D., Kang K.H., Lewis M.R., Nelson K.E., Methe B.A., Wu M., Heidelberg J.F., Paulsen I.T., Fouts D.E., Ravel J., Tettellin H., Ren Q., Read T.D., DeBoy R.T., Seshadri R., Salzberg S.L., Jensen H.B., Birkeland N.K., Nelson W.C., Dodson R.J., Grindhaug S.H., Holt I.E., Eidhammer I., Jonasen I., Vanaken S., Utterback T.R., Feldblyum T.V., Fraser C.M., Lillehaug J.R.,
       Detter J.C., Glavina T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Distributed under the Creative Commons Attribution-NoDerivs License
Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina Hammon N., Israni S., Pitluck S., Richardson P.; Seguencing of the draft genome and assembly of Rhodopseudomonas palustris BisA53."; to the BMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                       Submitted (OCT-2005) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Methylococcus capsulatus.
Bacteria; Proteobacteria; Gammaproteobacteria; Methylococcales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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                                                                                                                                                                                                                     Larimer F., Land M.; "Annotation of the draft genome of Rhodopseudomonas palustris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48.5%; Score 47; DB 2; Length 365; 50.0%; Pred. No. 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AALA01000029; EA087857.1; -; Genomic_DNA.
Hypothetical protein.
SEQUENCE 365 AA; 40239 MW; E11D3C9BC0F1244F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-NOV-2004, sequence version 1.
07-FEB-2006, entry version 9.
Hydrophobe/amphiphile Efflux-1 (HAE1) family protein.
OrderedLocusNames=MCA1360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-NOV-2004, integrated into UniProtKB/TrEMBL.
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GO; GO:0005215; F:transporter activity; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IPR001036; Acrflvin_res.
InterPro; IPR004764; HAEI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Mismatches
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                                                                                                                                                                                              US DOE Joint Genome Institute (JGI-ORNL);
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Best Local Similarity 50.00
Best Local 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 VDGQKATNIFPYTAPG
                                                                                                                                                                                                                                                                                                                                                                     preliminary data.
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Q9FYU1_CHLRE
Q9FYU1;
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                      SOLUTION DE LA DELLA DE LA COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCCO COCO CO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP clade,
Ehrhartoideae, Oryzeae, Oryza.
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                                                                                                                                                                           Gaps
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Buell C.R., Yuan Q., Ouyang S., Moffat K.S., Hill J.N., Gansberger I Brenner M., Burgess S., Hance M., Shvattsbeyn M., Tsitrin T., Riggs F., Haiao J., Ziamann V., Blunt S., Pai G., VanAken S.E., Utterback T.R., Feldblyum T.V., Quackenbush J., Salzberg S.L., White O., Fraser C.M.;

"Oryza sativa chromosome 3 BAC OSJNBa0077G22 genomic sequence.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
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Pred. No. 2.2e+02;
2; Mismatches 3; Indels
                                                                                                                              Length 1054;
                                                                                                                         48.5%; Score 47; DB 2; Length 105
56.2%; Pred. No. 1.5e+02;
ive 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1538 AA; 174629 MW; 5E7A521B398BC776 CRC64;
                                                                                   1054 AA; 115005 MW; BB032CB91B38D1A8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Buell R.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
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Gramene; Q94H26; -
GO; GO:000347; F:DNA binding; IEA.
GO; GO:0004223; F:ribonuclease H activity; IEA.
GO; GO:0015074; P:DNA integration; IEA.
InterPro; IPR005162; Retrotrans gag.
InterPro; IPR008166; Retrotrans gag.
InterPro; IPR008156; RNase.H.
InterPro; IPR001584; Rve.
Pfam; PP00075; RnaseH; 1.
Pfam; PP00075; RnaseH; 1.
Pfam; PP00065; rve; 1.
                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-2001, integrated into UniProtKB/TrEMBL. 01-DEC-2001, sequence version 1. 21-FEB-2006, entry version 18. Putative gag-pol polyprotein. Name=oSJNBa0077622.13;
                                                                                                                                                                                                                                                                                                                                                                      Q94126 ORYSA PRELIMINARY; PRT; 1538 AA.
Q94H26;
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Pfam; PF00873; ACR tran; 1.
PRINTS; PR00702; ACRIFLAVINRP.
TIGRFAMS; TIGR00915; 2A0602; 1.
                                                                                                                                                                                                                                                            294 VNGHKSTQIVVYTLPG 309
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740 VDGRAAVNIMPYT 752
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                                                                                                                                                  Best_Local Similarity 56.2
Matches 9; Conservative
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Matches 8; Conserv
                                                                 Complete proteome
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      iron hydrogenase of Chlamydomonas reinhardtii has a single ing domain containing an H-cluster catalytic center and lacking delectron carriers.";
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Happe T., Kaminski A.;
Happe T. Solation and characterization of the hydA gene encoding the Fe-
hydrogenase of Chlamydomonas reinhardtii.";
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                    Pe-hydrogenase precursor (EC 1.18.99.1) (Iron-hydrogenase HydAl). Name=hydl; Synonyms=hydA, hydAl; Chlamydomonas reinhardtii. Bukaryota, Viridiplantae; Chlorophyta; Chlorophyceae; Chlamydomonadales; Chlamydomonadales; Chlamydomonadales; Chlamydomonadales.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kaminski A.U., Happe T.; "Isolation and characterization of the hydA gene encoding the Fehydrogenase of Chlamydomonas reinhardtii."; Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ghirardi M.L., "The properties of the Chlamydomonas "Two putative Fe-only hydrogenases cloned from Chlamydomonas reinhardtii are coexpressed in Cells undergoing anaerobiosis."; Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
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Forestier M., Zhang L., Plummer S., Ahmann D., Seibert M.,
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GO; GO:0008901; F:electron transporter activity; IEA.
GO; GO:0016491; F:oxidoxin hydrogenase activity; IEA.
GO; GO:0016491; F:oxidoxeductase activity; IEA.
InterPro; IPR004108; Fe hyd Ig C.
InterPro; IPR003149; Fe hyd SGU.
Fean; PF02206; Fe hyd Ig C; I.
Ffam; PF02256; Fe hyd SGU; I.
Oxidoxeductase; Signal; Transit peptide.
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2E618A259E6572F4 CRC64;
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55.6%; Pred. No. 99;
:ive 2; Mismatches
                                                        01-MAR-2001, integrated into UniProtKB/TrEMBL 01-MAR-2001, sequence version 1. 07-FEB-2006, entry version 19.
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EMBL; AY05575; AAL23572.1; -; mRNA.
EMBL, AJ012098; CAC80065.1; -; mRNA.
EMBL; AJ018413; CAC83731.1; -; Genomic_DNA.
HSSP; P07598; 1HFE.
497 AA.
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   PRT;
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   PRELIMINARY;
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RESULT 10 P93168 SOYBN

RESULT

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EMBL; U55874; AAC09952.1; -; mRNA.
PIR; JW0071; JW0071.
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                                                                                                                                                                                            PRELIMINARY;
                                                                      11; Conservative
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Best Local Similarity
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Q42792;
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Q9SM55;
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042792 SOYBN
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Matches
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                                                                                                                                                                                                                                                                                                                             GO:0004066; F:asparagine synthase (glutamine-hydrolyzing). . .; IEA. GO:0016874; F:ligase activity; IEA. GO:0016872; P:asparagine biosynthesis; IEA. GO:0008152; P:metabolism; IEA.
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Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                               Glycine max (Soybean).
Wataryota, Viridiplantea, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons; core eudicotyledons; rosids; eurosids 1; Fabales; Fabaceae, Papilionoideae, Phaseoleae;
                                                                                                                                                                                                    Hughes C.A., Beard H.S., Matthews B.F., "Molecular cloning and expression of two CDNAs encoding asparagine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-NOV-2005, integrated into UniProtKB/TrEMBL.
22-NOV-2005, sequence version 1.
27-NOV-2006, entry version 3.
Asparagine synthetase.
Glycine max (Soybean).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14;
                                                                                                                                                                                          MEDLINE=97188563; PubMed=9037148; DOI=10.1023/A:1005784202450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 579;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lin S., Xiang W., Fan Z.;
Submitted (SEP-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               579 AA; 65366 MW; F7E80DA2019E0FC5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47.4%; Score 46; DB 2; I 34.4%; Pred. No. 1.2e+02; tive 2; Mismatches 5;
                      01-MAY-1997, integrated into UniProtKB/TrEMBL. 01-MAY-1997, sequence version 1. FBB-2006, entry version 26. Asparagine synthetase 1 (EC 6.3.5.4).
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 579 AA.
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Pfam; PF00310; GATase 2; 1.
TIGRFAMS; TIGR01536; asn synth AEB; 1
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 PRT;
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GO; GO:0006529; P:asparagine biosyr
GO; GO:0008152; P:metabolism; IEA.
InterPro; IPR006426; Asn_synth_AEB.
InterPro; IPR001962; Asn_synthase.
InterPro; IPR001963; GATase_2.
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Q38IA6;
                                                                                                                                                                                                                               synthetase in soybean.";
Plant Mol. Biol. 33:301-311(1997).
                                                                                                                                                                                                                                                                                                    EMBL; U77679; AAC49614.1; -; mRNA.
HSSP; P22106; 1CT9.
 PRELIMINARY;
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 P93168 SOYBN
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Yamagata H., Nakajima A., Bowler C., Iwasaki T.;
Wolecular cloning and characterization of a cDNA encoding asparagine synthetase from soybean (Glycine max L.) cell cultures.";
Biosci. Biotechnol. Biochem. 62:148-150(1998).
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Wataryora, Viridiplanteae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
GO; GO:0004066; F:asparagine synthase (glutamine-hydrolyzing). . . GO; GO:0006529; P:asparagine biosynthesis; IEA. GO; GO:00151; P:metabolism; IEA. SEQUENCE 579 AA; 65219 WW; 3F3A9F62EA447A17 CRC64;
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34.4%; Pred. No. 1.2e+02;
Miematiches 5;
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01-MAY-2000, sequence version 1.
07-FEB-2006, entry version 21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1996, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                            462 IDGLKAHAEKHVTDRMMLNAANİFPFNTPTTK 493
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Pfam; PF00713; Asn_synthase; 1.
TIGRFAMs; TIGRFAN5; TIGRFAN5; TIGRFAN5; TIGRFAN5.
PROSITE; PS00443; GATASE_TYPE_II; UNKNOWN_1.
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                                                                                                                                                                                                                 2; Mismatches
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Asparagine synthetase (EC 6.3.5.4).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR006426; Asn_synth AEB.
InterPro; IPR001962; Asn_synthase.
InterPro; IPR000583; GATase_2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DDI=10.1128/JB.184.16.4661-46f1.2002,
DDI=10.1128/JB.184.16.4661-46f1.2002,
Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.
Pernan N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
Etherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                     Asparagine synthetase (glutamine-hydrolyzing) 2. /Frid=PRO_0000056923.
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Glutamine amidocransferase.
GATase (By similarity).
FS6DCA2015F73451 CRC64;
                                                                                                                                                                                                              Pfam; PF00733; Asn. synthase; 1.
Pfam; PF00733; Asn. synthase; 1.
Pfam; PF00310; GATase 2; 1.
TIGRPAMs; TIGR01536; asn. synth AEB; 1.
PROSITE; PS00443; GATASE_TYPE_II; 1.
Amino-acid biosynthesis; Asparagine biosynthesis; Glutamine amidotransferase; Ligase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47.4%; Score 46; DB 1; I ilarity 31.2%; Pred. No. 1.2e+02; Conservative 4; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-WAR-2003, integrated into UniprotKB/TrEMBL. 01-WAR-2003, sequence version 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, AE013929; AAM86837.1; -; Genomic_DNA.
BioCyc; YPES187410:73288-MONOMER; -.
GO; GO:0019867; C:outer membrane; IEA.
GO; GO:0019867; C:outer membrane; IEA.
InterPro; IPR006840; HEP Hag.
InterPro; IPR005594; YadA.
InterPro; IPR05594; YadA.
Pfam; PF056662; HEP, Hag.
Pfam; PF056662; HEP, Hag.
Pfam; PF056662; HEP, Hag.
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J. Bacteriol. 184:4601-4611(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY; PRT;
                                                                                                                                             InterPro; IPR006426; Asn synth AEB.
InterPro; IPR001962; Asn synthase.
InterPro; IPR00583; GATase_2.
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MEDLINE=22137863; PubMed=12142430;
                                                                              EMBL, X89410; CAA61590.1; -; mRNA.
PIR; S69183; S69183.
HSSP; P22106; 1CT9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 585 AA; 65839 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Enterobacteriaceae; Yersinia.
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es 10; Conserv
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                                                                                                                                                                                                                                                                                                                                  Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae; Lotus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plant Mol. Biol. 30:883-897 (1996).
-!- CATALYTIC ACTIVITY: ATP + L-aspartate + L-glutamine = AMP + diphosphate + L-asparagine + L-glutamate.
-!- PATHWAY: Asparagine biosynthesis.
-!- SIMILARITY: Contains 1 asparagine synthetase domain.
-!- SIMILARITY: Contains 1 type-2 glutamine amidotransferase domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                         Phaseolus vulgaris (Kidney bean) (French bean).

Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosida; eurosida I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;

Phaseolus.
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07-FEB-2006, entry version 39.
Asparagine synthetase [glutamine-hydrolyzing] 2 (BC 6.3.5.4)
                                                                                                                                                                                                                        STRAIN=Great Northern; TISSUE=Root;
Galvez-Valdivieso G., Osuna D., Perez-Vicente R., Pineda M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 579;
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34.4%; Pred. No. 1.2e+02;
ive 2; Mismatches 5; Indels
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MEDLINE=96270368; PubMed=8639748;
Waterhouse R.N., Smyth A.J., Massoneau A., Prosser I.M.,
                                                                                                                                                                                                                                                                                         Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      579 AA; 65266 MW; 7A74F5AE852CE2E6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1996, integrated into UniProtKB/Swiss-Prot.
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Asparagine synthetase (Type-I) (EC 6.3.5.4).
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HSSP; P22106; 1CT9.
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Conservative 2
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                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE.
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Best Local Similarity
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                                                                                                                                                         NCBI_TaxID=3885;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clarkson D.T.;
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Gaps

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Hypothetical protein.
SEQUENCE 641 AA; 62094 MW; A5951553FEE45162 CRC64;
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ô 0; Gaps Query Match 47.4%; Score 46; DB 2; Length 641; Best Local Similarity 52.9%; Pred. No. 1.3e+02; Matches 9; Conservative 3; Mismatches 5; Indels

¹ VDGQKAINIFPYTAPGT 17 | ::|||||| | | | 82 INGQKAINLAPATISST 98 දු ද

Search completed: August 30, 2006, 04:29:13 Job time: 74.1818 secs

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Sequence 2960, Ap
Patent No. 5256558
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Sequence 2, Appli
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88.424 Million cell updates/sec
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| RWC Celerra SIDS3/ptodata/2/iaa/5 COMB.pep:*
| EMC Celerra SIDS3/ptodata/2/iaa/6 COMB.pep:*
| FWC Celerra SIDS3/ptodata/2/iaa/f COMB.pep:*
| RWC Celerra SIDS3/ptodata/2/iaa/H COMB.pep:*
| RWC Celerra SIDS3/ptodata/2/iaa/H COMB.pep:*
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Sequence 10,
Sequence 3000
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Sequence 7
Sequence 3
Sequence 4
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-08-36-58-2

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US-09-401-636-3

US-09-401-636-3

US-09-401-636-9

US-09-401-636-9

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US-09-401-636-9

US-09-401-636-9

US-09-401-636-9

US-09-401-636-10

US-09-401-636-10

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US-09-107-433-2960
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                       OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                      1 VDGQKATNIFPYTAPGTK 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              length: 0
length: 2000000000
                                                                                                                                                                                                                                                                                                                                                 US-10-758-165A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query
Match Length DB
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Maximum DB seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Database
                                                                                                                                                                                                         Run on:
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Sequence 4212, Ap	Sequence 10, Appl	Patent No. 5256558	Sequence 12884, A	Sequence 6, Appli	Sequence 66, Appl	Sequence 6, Appli	Sequence 66, Appl	Sequence 6, Appli	Sequence 66, Appl	Sequence 8106, Ap	Sequence 1, Appli	Sequence 7, Appli	Sequence 1, Appli	Sequence 7, Appli	Sequence 26880, A	Sequence 4924, Ap	Sequence 27624, A	Sequence 29, Appl
US-09-134-001C-4212	US-08-840-767-10	5256558~2	US-09-902-540-12884	US-09-993-777-6	US-09-993-777-66	US-09-994-064-6	US-09-994-064-66	PCT-US96-03916-6	PCT-US96-03916-66	US-09-489-039A-8106	US-08-967-364-1	US-08-967-364-7	US-09-368-408-1	US-09-368-408-7	US-09-252-991A-26880	US-09-543-681A-4924	US-09-252-991A-27624	US-09-612-402B-29
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132	475	586	557	985	985	985	985	985	985	232	570	570	570	570	1364	464	608	63
45.4	44.3	44.3	43.3	43.3	43.3	43.3	43.3	43.3	43.3	42.3	42.3	42.3	42.3	42.3	42.3	41.8	41.8	41.2
44	43	43	42	42	42	42	42	42	42	41	41	41	41	41	41	40.5	40.5	40
27	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

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'Xaa' at location 81 stands for Lys, Arg, Thr, Met, Glu, Gly, Val, Gln, Pro, Leu, a stop codon, Trp, or Ser.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: misc feature
LOCATION: (82). (82)
OTHER INFORMATION: The 'Xaa' at location 82 stands for a stop codon, Trp, or Cys.
                                                                                                                       US-09-281-760E-35

| US-09-281-760E-35 | Sequence 35, Application US/09281760E |
| Patent No. 6734287 |
| Patent No. 6734287 |
| APPLICANT: Werner, Brion |
| APPLICANT: Francour, Gree |
| TITLE OF INVENTION: Specific Binding Protein for Treating |
| TITLE OF INVENTION: Canine Allergy |
| FILE REPRENCE: 01-1275A |
| CURRENT FILING DATE: 1999-03-30 |
| PRIOR PILICATION NUMBER: US/09/281,760E |
| WUMBER OF SEQ ID NOS: 39 |
| SOFTWARE: FastSEQ for Windows Version 3.0 |
| SEQ ID NO 35 |
| LENGTH: 108 |
| TENDER OF TREATHS |
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NAME/KEY: misc_feature
LOCATION: (413)..(414)
OTHER INFORMATION: "n" stands for any nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: misc feature
LOCATION: (136)..(136)
OTHER INFORMATION: "n" stands for any nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc feature
LOCATION: (451)..(451)
OTHER INFORMATION: "n" stands for any nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: (460)..(462)
OTHER INFORMATION: "n" stands for any nucleic acid
PEATURE:
ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Canis familiaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc feature
LOCATION: (81)...(81)
OTHER INFORMATION: The '
OTHER INFORMATION: Ala,
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LOCATION: (500)..(500)
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146 VDGQKATNIFPYTAPGTK 163
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  48 VDGQKATNIFPYTAPGTK 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               426 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                             NEW JERSEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: si
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-336-583-2
                                                                              US-08-336-583-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09701623C
Patent No. 6811782
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL SEPERATOR OF THE TREATMENT OF TITLE OF INVENTION: ALLERGY
TITLE OF INVENTION: ALLERGY
TITLE REFERENCE: 11514153US1
CURRENT APPLICATION NUMBER: US/09/701,623C
CURRENT FILING DATE: 1299-06-21
PRIOR APPLICATION NUMBER: 09/100,287
PRIOR APPLICATION NUMBER: 09/100,287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 97; DB 2; Length 10
100.0%; Pred. No. 3.6e-08;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                  FEATURE:
NAME/KEY: misc_feature
LOCATION: (847)..(849)
OTHER INFORMATION: "n" stands for any nucleic acid
                                                                                                                                                                                                                                                                                                                                                PEATURE:
NAME/KEY: misc_feature
LOCATION: (1382)
OTHER INFORMATION: "n" stands for any nucleic acid
                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: misc_feature
LOCATION: (853)..(853)
OTHER INFORWATION: "n" stands for any nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
i LOCATION: (1832)..(1832)
j: OTHER INFORMATION: "n" stands for any nucleic acid
US-09-281-760E-35
OTHER INFORMATION: "n" stands for any nucleic acid
                                                           LOCATION: (530)..(530)
OTHER INFORMATION: "n" stands for any nucleic acid
                                                                                                                    NAME/KEY: misc feature
LOCATION: (568)..(568)
OTHER INFORMATION: "n" stands for any nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 97; DB 2; I 100.0%; Pred. No. 1.1e-07; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: CH2CH3n of dog 1gE PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 VDGQKATNIFPYTAPGTK 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47 VDGQKATNIFPYTAPGTK 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 VDGQKATNIFPYTAPGTK 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 91
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS: Patel,
JOURNAL: Immunogenetics
                                      NAME/KEY: misc feature LOCATION: (530)..(530)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VOLUME: 41
PAGES: 282-286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Dog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , DATE: 1995
US-09-701-623C-2
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Gaps
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Sequence 2, Application PC/TUS9513795

GENERAL INFORMATION:

APPLICANT: PATEL, MAYUR D.

TITLE OF INVENTION: DA ENCODING CANINE IMMUNOGLOBULINS

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: CARTY

STREET: 1.26 E. LINCOLN AVENUE; P.O. BOX 2000

CITY: RAHMAY
Sequence 2, Application US/08336583
Patent No. 5629415
GENERAL INFORMATION:
APPLICANT: PATEL, MAYUR D.
TILLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULIN INDMERS OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSE: CHRISTINE E. CARTY
STREET: 126 B. LINCOLN AVENUE
CITY: RAHMAY
                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION UNMER: US/08/336,583
FILING DATE: 09-NOV-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: CARTY CHRISTINE E.
REGISTRATION NUMBER: 36,099
REFERENCE/DOCKET NUMBER: 19211
TELEPHONE: (908) 594-6734
TELEPHONE: (908) 594-4720
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07065-0907
COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING: STEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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1 VDGQKATNIFPYTAP 15
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Felis catus
US-09-479-614-2
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Patent No. 657372

GENERAL INFORMATION:
APPLICANT: McCall, Catherine
APPLICANT: Weber, Eric
TITLE OF INVENTION: Peline Immunoglobulin E Molecules and Related Methods
FILE REFERENCE: P-1047

CURRENT APPLICATION NUMBER: US/09/479,614

CURRENT PILING DATE: 2000-01-07

EARLIER FILING DATE: 1999-01-07

EARLIER FILING DATE: 1999-01-07

SEALIER PILING DATE: 1999-01-07

SEALIER PILING DATE: 1999-01-07

SEALIER PLING DATE: 1999-01-07

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APPLICANT: WcCall, Exic
TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
TITLE OF INVENTION: Peline Immunoglobulin E Molecules and Related Methods
FILE REFERENCE: P-1047
CURRENT APPLICATION NUMBER: US/09/479,614
CURRENT FILING DATE: 2000-01-07
EARLIER APPLICATION NUMBER: 60/115,033
EARLIER FILING DATE: 1999-01-07
NUMBER OF SEQ ID NOS: 34
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13795
                                                    CLASSIFICATION:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: CARTY, CHRISTINE E.
REGISTRATION NUMBER: 36,099
REFERENCE/DOCKET NUMBER: 19211Y
TELEPHONE: (908) 594-6734
TELEPHONE: (908) 594-6734
TELEPHONE: (908) 594-4720
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 426 amino acids
TYPE: amino acid
STARNBEDBESS: single
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100.0%; Pre
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Best Local Similarity 100.
Matches 18; Conservative
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ORGANISM: Felis catus
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Best Local Similarity
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                                         FILING DATE:
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US-09-479-614-14
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US-09-479-614-2
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WS-09-479-614-29

WS-09-479-614-29

Sequence 29, Application US/09479614

Patent No. 6573373

GENERAL INFORMATION:

APPLICANT: Weber, Eric

TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods

FILE REFERENCE: P-1047

CURRENT APPLICATION NUMBER: US/09/479,614

CURRENT PILING DATE: 2000-01-07

EARLIER APLICATION NUMBER: 05/015,033

EARLIER FILING DATE: 1999-01-07

WUMBER: OF SEQ ID NOS: 34

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 29

LENGTH: 496

TYPE: PRT

CORANISM: Felis catus
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            Length 496;
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US-09-401-636-7
Score 87; DB 2; Le
Pred. No. 7.2e-06;
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86.7%; Pred. No. 0.00086;
iive 1; Mismatches 1;
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Sequence 7, Application US/09401636

Patent No. 6913749

GENERAL INFORMATION:

APPLICANT: Hellman, Lars T.

TITLE OF INVENTION: ENHANCED VACCINES

FILE REFERENCE: 1023/006001

CURRENT PELING DATE: 1999-09-22

PRIOR APPLICATION NUMBER: US 60/106,652

PRIOR APPLICATION NUMBER: US 60/106,652

PRIOR APPLICATION NUMBER: US 60/106,652

PRIOR APPLICATION NUMBER: US 60/106,652

PRIOR APPLICATION NUMBER: US 60/106,652

FRIOR SEQ ID NOS: 11

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 7

LENGTH: 343

TYPE: PRI

ORGANISM: Artificial Sequence
                                                          Mismatches
       Query Match
Best Local Similarity 100.0%; Pr
Matches 16; Conservative 0;
                                                                                                                              216 VDGQKATNIFPYTAPG 231
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Best Local Similarity 86.73
Matches 13; Conservative
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 76.93
Matches 10; Conservative
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62 VDGQEAENLFPYT 74
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59.8%; Score 58; DB 2; Length 341;
Best Local Similarity 76.9%; Pred. No. 0.22;
Matches 10; Conservative 2; Mismatches 1; Indels
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, OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-4
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US-09-401-636-3
                                                                  US-09-401-636-3
US-09-401-636-3
US-09-401-636-3
Sequence 3, Application US/09401636
Patent No. 6913749
GENERAL INFORMATION:
TITLE OF INVENTION: ENHANCED VACCINES
FILE REFERENCE: 10223/006001
CURRENT APPLICATION NUMBER: US/09/401,636
CURRENT APPLICATION NUMBER: US 60/106,652
PRIOR PILING DATE: 1998-11-02
NUMBER OF SEQ ID NOS: 11
SOUTHWARE: FASTERE for Windows Version 4.0
SEQ ID NO 3
LENGTH: 341
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APPLICANT: Hellman, Lars T.
TITLE OF INVENTION: ENHANCED VACCINES
FILE REFERENCE: 10223/006001
CURRENT APPLICATION NUMBER: US/09/401,636
CURRENT FILING DATE: 1999-09-22
PRIOR FILING DATE: 1998-11-02
PRIOR FILING DATE: 1998-11-02
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
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US-09-401-636-4
Sequence 4, Application US/09401636
; Partent No. 6913749
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61 VDGQKAENLFPYTAP 75
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Best Local Similarity 76.>
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62 VDGQEAENLFPYT 74
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62 VDGQEAENLFPYT 74
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LENGTH: 341
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US-09-401-636-9
Sequence 9, Application US/09401636
Patent No. 6913749
GENERAL INFORMATION:
APPLICANT: Hellman, Lars T.
TITLE OF INVENTION: ENHANCED VACCINES
FILLE REFERENCE: 10223/006001
CURRENT APPLICATION NUMBER: US/09/401,636
CURRENT FILING DATE: 1999-09-22
PRIOR FILING DATE: 1998-11-02
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FESTEREQ for Windows Version 4.0
SEQ ID NO 9
LENGTH: 341
CURRENT APPLICATION WUMBER: US/09/401,636
CURRENT FILING DATE: 1999-09-22
PRIOR APPLICATION NUMBER: US 60/106,652
PRIOR FILING DATE: 1998-11-02
PRIOR FILING DATE: 1998-11-02
SPINMER OF SEQ ID NOS: 11
SOFTWARE: FRRESEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 341
TYPE: DOT
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Sequence 11, Application US/09401636

Patent No. 6913749

GENERAL INFORMATION:

TITLE OF INVENTION:

TITLE OF INVENTION:

FILE REPERENCE: 10223/006001

CURRENT FILING DATE: 1999-09-22

PRIOR APPLICATION NUMBER: US 60/106,652

PRIOR APPLICATION NUMBER: US 60/106,652

PRIOR APPLICATION NUMBER: US 60/106,652

PRIOR PILING DATE: 1999-11-02

NUMBER OF SEQ ID NOS: 11

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 11

TYPE: PRI

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                                                                                                              Score 58; DB 2; Length 341;
Pred. No. 0.22;
2; Mismatches 1; Indels
; OTHER INFORMATION: Synthetically generated proteins US-09-401-636-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Synthetically generated proteins US-09-401-636-5
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                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
US-09-401-636-5
Sequence 5, Application US/09401636
Patent No. 6913749
GENERAL INFORMATION:
APPLICANT: Hellman, Lars T.
TITLE OF INVENTION:
FILE REFERENCE: 10223/006001
CURRENT APPLICATION NUMBER: US/09/401,636
CURRENT FILING DATE: 1999-09-22
PRIOR APPLICATION NUMBER: US/09/401,636
PRIOR FILING DATE: 1999-10-22
NUMBER OF SEQ ID NOS: 11
SOFTHARE: FASESEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 342
TUPNED: DATE: 1998-11-02
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; Sequence 8, Application US/09401636
; Sequence 8, Application US/09401636
; Patent No. 6313749
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT PILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR PILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 342

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ORGANISM: Artificial Sequence
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                                                                                                          Query Match
Best Local Similarity 76.9%;
Matches 10; Conservative
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62 VDGQEAENLFPYT 74
                                                                                                                                                                                                                                                             1 VDGQKATNIFPYT 13
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Best Local Similarity 76.9
Matches 10; Conservative
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Sequence 10, Appl
Sequence 14, Appl
Sequence 24, Appl
Sequence 29, Appl
Sequence 27, Appl
Sequence 27, Appl
Sequence 7, Appl
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Sequence 7, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 6, Appl
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Sequence 11, Appl
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Sequence 11, Appl
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Sequence 13, Appli
Sequence 14, Appli
Sequence 14, Appli
Sequence 6, Appli
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1. /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2. /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

3. /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

4. /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

5. /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

6. /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
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                                                                      August 30, 2006, 04:33:28; Search time 90.9091 Seconds (without alignments) 91.717 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description
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GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-758-165-9
US-10-723-207-2
US-10-723-207-2
US-10-758-165-10
US-09-479-614-14
US-09-479-614-29
US-09-479-614-29
US-10-214-524-25
US-10-409-772-2
US-10-409-772-2
US-10-409-772-2
US-10-409-772-2
US-10-43-31-64-7
US-10-43-31-64-7
US-10-43-31-64-12
US-10-43-31-64-12
US-10-43-31-6-6
US-10-43-31-6-6
US-10-43-31-6-6
US-09-401-636-4
US-09-401-636-4
US-09-401-636-6
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US-10-176-664-3
US-10-176-664-4
US-10-176-664-6
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Maximum Match 100%
Listing first 45 summaries
                                                   OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Match Length DB
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Sequence 9, Appli
Sequence 11, Appl
Sequence 5, Appli
Sequence 8, Appli
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US-10-176-664-9
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US-10-673-594-4
US-10-673-594-6
US-10-673-594-9
US-10-673-594-9
US-10-673-594-19
US-09-401-636-8
US-09-401-636-8
US-10-176-664-8
US-10-176-664-8
US-10-673-594-8

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ALIGNMENTS

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US-10-73-207-2

1 Sequence 2, Application US/10723207

2 Sequence 2, Application US/10723207

3 Equence 2, Application US/10723207

4 PUBLICANT: Walfield, Alan M.

5 TITLE OF INVENTION: PEPTICE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF TITLE OF INVENTION: PAPPLICANT: WALFIELD, ALLERGY.

7 TITLE OF INVENTION: PAPPLICATION OF ALLERGY.

8 FILE REFERENCE: 1151-4153US.

7 CURRENT APPLICATION NUMBER: 02/10/1.623

8 PRIOR FILING DATE: 2003-11-24

9 PRIOR FILING DATE: 2003-11-24

9 PRIOR FILING DATE: 1999-06-21

9 PRIOR FILING DATE: 1999-06-21

9 PRIOR FILING DATE: 1999-06-20

10 NUMBER OF SEQ ID NOS: 91

11 SOFTWARE: PALENTIN Ver. 2.1
WS-10-758-165-9
; Sequence 9, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:
; TILLS OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; TILLS OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; CURRENT APPLICATION NUMBER: US/10/758,165
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR APPLICATION NUMBER: US 60/440,472
; ROFTHARE PRESE PATENTING DATE: 2003-01-16
; SOFTWARE PATENTING DATE: 2003-01-16
; SEQ ID NO 9
; SEQ ID NO 9
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Pred. No. 1e-08;
; Mismatches 0; Indels
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Best Local Similarity 100.0%;
Matches 18; Conservative 0
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ORGANISM: Canis familiaris
US-10-758-165-9
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Sequence 28, Application US/10214524

Publication No. US20030073142A1

GENERAL INFORMATION:
APPLICANT: Vang. Yong-Min

APPLICANT: Chen, Swey-Shen Alex
APPLICANT: Chen, Swey-Shen Alex
APPLICANT: Chen, Shong
ITILE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF
ITILE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF
CURRENT APPLICATION NUMBER: US/10/214,524

CURRENT FILING DATE: 2002-08-08
PRIOR APPLICATION WINBER: 60/312,120

PRIOR APPLICATION WINBER: 60/312,120

NUMBER OF SEQ ID NOS: 61

SEQ ID NO 28

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US-10-758-165-10
Sequence 10, Application US/10758165
Publication No. US20050196816A1
SEGNERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
TITLE OF INVENTION: US/10/758,165
CURRENT APPLICATION NUMBER: US/10/758,165
CURRENT PILING DATE: 2004-01-16
SPATOR FILING DATE: 2003-01-16
NUMBER OF SEQ ID NOS: 16
NUMBER OF SEQ ID NOS: 16
SSOFTWARE: Patentin version 3.2
LENGTH: 18
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                                                                                                                                     CTHER INFORMATION: CH2CH3n of dog IgE
PUBLICATION INFORMATION:
AUTHORS: Patel,
OUGUNAL: Immunogenetics
VOLUME: 41
PAGES: 282-286
DATE: 1995
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, ORGANISM: Dog (Canis familiaris)
US-10-214-524-28
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Best Local Similarity 100.
Matches 18; Conservative
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US-10-758-165-10
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                                                                  ORGANISM: Dog
LENGTH: 312
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RESULT 6
US-10-409-772-14

Sequence 14, Application US/10409772

Publication No. US2030216565A1

Sequence 114, Application US/10409772

Publication No. US2030216565A1

SENDEAL INFORMATION:
APPLICANT: Weber, Eric

TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods

FILE REFERENCE: P-1047

CURRENT FAPLICATION NUMBER: US/10/409,772

CURRENT FILING DATE: 2000-01-07

PRIOR FILING DATE: 2000-01-07

NUMBER OF SEQ ID NOS: 34

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                           US-09479-614-14
US-09479-614.4
US-09479-614.4
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US-09479-614.4
US-0878-1 US-0878-108.4
US-0878-1 US-0878-108.4
US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US-0878-1 US
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100.0%; Pred. No. 1.4e-05;
tive 0; Mismatches 0; Indels
        Length 18;
        DB 5; Le
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Query Match 89.7%; Score 87; DB Best Local Similarity 100.0%; Pred. No. 4.4 Matches 16; Conservative 0; Mismatches
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US-09-479-614-2
; Sequence 2, Application US/09479614
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Best Local Similarity 100.0
Matches 16; Conservative
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Best Local Similarity 100.0
Matches 16; Conservative
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; ORGANISM: Felis catus
US-09-479-614-14
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 25
LENGTH: 496
TYPE: PRT
                                                                                   ; ORGANISM: Cat (Felis catus)
US-10-214-524-25
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; LENGTH: 496
; TYPE: PRT
; ORGANISM: Felis catus
US-10-409-772-29
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TYPE: PRT
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Sequence 25, Application US/10214524

Sequence 25, Application US/10214524

Publication No. US20030073142A1

GENERAL INFORMATION:
APPLICANT: Chen, Swey-Shen Alex
APPLICANT: Barankiewicz, Theresa J.
APPLICANT: Chen, Zhong
TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF
TITLE OF INVENTION: UNMORER: US/10/214,524

CURRENT APPLICATION NUMBER: US/10/214,524

CURRENT FILING DATE: 2002-08-08

PRIOR APPLICATION NUMBER: 60/312,120

NUMBER OF SEQ ID NOS: 61
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Publication No. US20030013183A1
GENERAL INFORMATION:
APPLICANT: McCall. Catherine
APPLICANT: WcCall. Catherine
APPLICANT: Weber, Eric
TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
FILE REFERENCE: P-1047
CURRENT APPLICATION NUMBER: US/09/479,614
CURRENT PILING DATE: 2000-01-07
EARLIER APPLICATION NUMBER: 60/115,033
EARLIER APPLICATION NUMBER: 60/115,033
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
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CURRENT PELICATION NUMBER: US/09/479,614
CURRENT FILING DATE: 2000-01-07
EARLIER APPLICATION NUMBER: 60/115,033
EARLIER PILING DATE: 1999-01-07
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 29
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Sequence 29, Application US/09479614
Publication No. US20030013183A1
GENERAL INFORMATION:
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Best Local Similarity 100.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16; Conservative
                                                                                                                                                                                                                                                               LENGTH: 496
TYPE: PRT
ORGANISM: Felis catus
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ORGANISM: Felis catus
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| Sequence 2, Application US/10409772
| Publication No. US20030216565A1
| GENERAL INFORMATION:
| APPLICANT: McDall, Catherine
| APPLICANT: Weber, Eric
| TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
| CURRENT APPLICATION NUMBER: US/10/409,772
| PRIOR APPLICATION NUMBER: US/09/479,614
| PRIOR PILING DATE: 2000-01-07
| NUMBER OF SEQ ID NOS: 34
| SOFTWARE: Patentin Ver. 2.0
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Sequence 29, Application US/10409772

Publication No. US20030216565A1

Publication No. US20030216565A1

APPLICANT: Meber. Eric

TITLE OF INVENTION: Faic

TITLE OF INVENTION: Faic

CURRENT APPLICATION NUMBER: US/10/409,772

CURRENT APPLICATION NUMBER: US/09/479,614

PRIOR APPLICATION NUMBER: US/09/479,614

PRIOR APPLICATION NUMBER: US/09/479,614

NUMBER OF SEQ ID NOS: 34

SOFTWARE: Patentin Ver. 2.0
                                                    Gaps
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  Length 496;
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Query Match
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 16; Conservative 0; Mismatches 0;
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89.7%; Score 87; DB
Best Local Similarity 100.0%; Pred. No. 1.6
Matches 16; Conservative 0; Mismatches
                                                                                                                                  216 VDGQKATNIFPYTAPG 231
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216 VDGQKATNIFPYTAPG 231

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75.3%; Score 73; DB 3; Length 343;
Best Local Similarity 86.7%; Pred. No. 0.0022;
Matches 13; Conservative 1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Synthetically generated proteins US-10-176-664-7
                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Synthetically generated proteins US-09-401-636-7
Sequence 7, Application US/09401636;
Sequence 7, Application US/09401636;
Patent No. US20010038843A1;
GENERAL INFORMATION:
APPLICANT: Hellman, Lars T.
TITLE OF INVENTION: ENHANCED VACCINES
FILE REFERENCE: 10223/006001
CURRENT FILING DATE: 1999-09-22;
PRIOR PELICATION NUMBER: US 60/106,652;
PRIOR FILING DATE: 1998-11-02;
NUMBER OF SEQ ID NOS: 11
SOUTHWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
LEMCHH: 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: ENHANCED VACCINES
FILE REPERENCE: 10223/006001
CURRENT APPLICATION NUMBER: US/10/176,664
CURRENT FILING DATE: 2002-06-19
PRIOR APPLICATION NUMBER: US/09/401,636
PRIOR APPLICATION NUMBER: US 60/106,652
PRIOR PILING DATE: 1999-09-22
PRIOR PILING DATE: 1999-01-22
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
LENGTH: 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7, Application US/10176664; Publication No. US20030031663A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/10673594 Publication No. US20040076625A1 GENERAL INFORMATION: APPLICANT: Hellman, Lars T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Artificial Sequence
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61 VDGQKAENLFPYTAP 75
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61 VDGQKAENLFPYTAP 75
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Best Local Similarity 86.7
Matches 13; Conservative
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US-10-673-594-7
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US-10-214-524-29

Sequence 29, Application US/10214524

Publication No. US20030073142A1

GENERAL INFORMATION:
APPLICANT: Chen, Swey-Shen Alex
APPLICANT: Chen, Shey-Shen Alex
APPLICANT: Chen, Zhong
TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF
TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF
CURRENT APPLICATION NUMBER: US/10/214,524

CURRENT TILING DATE: 2002-08-08

PRIOR PILING DATE: 2001-08-13

NUMBER OF SEQ ID NOS: 61

SOFTWARE: Patentin version 3.1

SEQ ID NO 29

LENGTH: 577
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75.3%; Score 73; DB 4; Length 577; 86.7%; Pred. No. 0.0038;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Duckbilled platypus (Ornithorhynchus anatinus)
US-10-214-524-29
                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Synthetically generated proteins US-10-673-594-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
TITLE OF INVENTION: ENHANCED VACCINES
FILE REFERENCE: 10223/00601
CURRENT APPLICATION NUMBER: US/10/673,594
CURRENT FILING DATE: 2003-09-29
PRIOR APPLICATION NUMBER: US/09/401,636
PRIOR APPLICATION NUMBER: US 60/106,652
PRIOR APPLICATION NUMBER: US 60/106,652
PRIOR FILING DATE: 1998-11-02
NUMBER OF SEQ ID NOS: 11
SEQ ID NO 7
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: August 30, 2006, 05:13:00 Job time : 91.9091 secs
                                                                                                                                                                                                                                                      LENGTH: 343
TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 86.74
Matches 13; Conservative
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14312, A 261230, A 261230, A 1125597, A 11313131313131313131315, A 11315, A 11316, A 11316, A 11316, A 11316, A 11316, A 11316, A 11316, A 11316, A 11316, A

22932,' A 54493, A 4930, Ap

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; Publication No. US20060159563A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; TILE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53629)B
; CURRENT APPLICATION NUMBER: US/11/330,403
; CURRENT FILING DATE: 2006-01-12
; NUMBER OF SEQ ID NOS: 19250
; SEQ ID NO 3689
; LENOTH: 239
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Publication No. US20060159563A1
GENERAL INPORMATION:
APPLICANT: Abad, Mark S.
TITLE OF INVENTION: Genes and Uses for Plant Improvement;
FILE REPRENCE: 38-21(5529)B
CURRENT APPLICATION NUMBER: US/11/330,403
CURRENT FILING DATE: 2006-01-12
NUMBER OF SEQ ID NOS: 19250
LENGTH: 80
US-11-330-403-14312
US-11-330-403-15230
US-11-330-403-15230
US-11-330-403-12597
US-11-355B-11318
US-10-449-902-30331
US-10-449-902-3031318
US-10-449-902-3031318
US-11-056-355B-11316
US-11-056-355B-11316
US-11-056-355B-1317
US-11-056-355B-5494
US-11-056-355B-5494
US-11-056-355B-5494
US-11-056-355B-35016
US-11-056-355B-35016
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US-11-056-355B-54493
US-10-953-349-4930
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: DCATION: (1)..(239)

: OTHER INFORMATION: unsure at all Xaa locations

US-11-330-403-3689
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ORGANISM: Glycine max
FEATURE:
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    US-11-330-403-2450
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3689, Ap
117777, Ap
2402, Ap
6386, Ap
118232, A
1293, Ap
7358, Ap
7358, Ap
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14971, A
5521, Ap
482, App
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14969, A
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                                                                                                                                                   August 30, 2006, 04:34:57 ; Search time 9.27273 Seconds (without alignments) 133.695 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Published Applications AA New:*

1: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pep:*

2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
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Sequence 1
Sequence 1
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Sequence 1
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                         GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-11-330-403-3689
US-11-330-403-15600
US-11-330-403-2402
US-11-330-403-2402
US-11-330-403-1386
US-11-330-403-18232
US-11-330-403-18232
US-11-330-403-18232
US-11-330-403-18232
US-11-330-403-18232
US-11-330-403-14971
US-11-330-403-482
US-11-330-403-482
US-11-330-403-14971
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US-11-330-403-14971
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US-11-330-403-14971
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US-11-330-403-14999
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.11-330-403-15095
                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                   250042 segs, 68872936 residues
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Maximum Match 1008
Listing first 45 summaries
                                                                                                            OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                      1 VDGQKATNIFPYTAPGTK 18
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Maximum DB seq length: 200000000
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97
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Match
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Score

Result

Gaps

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; ORGANISM: Glycine max US-11-330-403-2402
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Matches
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                14;
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                                                                                                                                                              ; General 156.00, Application US/11330403
; Publication No. US20060159563A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; TILLE REFERENCE: 38-21 (35629) B
; CURRENT APPLICATION NUMBER: US/11/330,403
; CURRENT FILING DATE: 2006-01-12
; NUMBER OF SEQ ID NOS: 19250
; SEQ ID NO 15600
; LENGTH: 250
                                                                                                                                                                                                                                                                                                                                                                                                                                             47.4%; Score 46; DB 7; Length 250; ilarity 34.4%; Pred. No. 3.2; Conservative 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-11-330-403-17777, Application US/11330403
; Sequence 17777, Application US/11330403
; Publication No. US20060159563A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53629)B
; CURRENT APPLICATION NUMBER: US/11/330,403
; CURRENT FILING DATE: 2006-01-12
; NUMBER OF SEQ ID NOS: 19250
; SEQ ID NO 17777
; LENGTH: 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch
1 Similarity 34.4%; Score 46; DB 7; Length 287;
1 Similarity 34.4%; Pred. No. 3.7;
11; Conservative 2; Mismatches 5; Indels
                Indels
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Publication No. US20060159563A1
GENERAL INFORMATION:
APPLICANT: Abad, Mark S.
TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REFERENCE: 38-21(53629)B
CURRENT APPLICATION NUMBER: US/11/330,403
CURRENT PILING DATE: 2006-01-12
SEQ ID NOS: 19250
LENGTH: 579
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                                                -ATNIFPYTAPGTK 18
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Pred. No. 3;
2; Mismatches
34.48;
                11; Conservative
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ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 11; Conserva
                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Glycine max
US-11-330-403-15600
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Matches 11; Conserv
Best Local Similarity
                                                1 VDGQK---
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US-11-330-403-2402
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    DB 7; Length 579;
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Sequence 6386, Application US/11330403
Publication No. US20060159563A1
GENERAL INFORMATION:
APPLICANT: Abad, Mark S.
TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REFERENCE: 38-21(53629)B
CURRENT APPLICATION NUMBER: US/11/330,403
CURRENT APPLICATION NUMBER: US/11/330,403
NUMBER OF SEQ ID NOS: 19250
SEQ ID NO 6386
FIND TENDER OF SEQ ID NOS: 19250
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Publication No. US20060159563A1
Publication No. US20060159563A1
Publication No. US20060159563A1
Publication No. US20060159563A1
APPLICANT: Abad, Mark S.
TITLE OF INVENTION: Genes and Uses for Plant Improvement FILE REFERENCE: 38-21(53529)B
CURRENT APPLICATION NUMBER: US/11/330,403
CURRENT FILING DATE: 2006-01-12
SEQ ID NO. 11265
LENGTH: 579
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; Sequence 1822, Application US/11330403
; Publication No. US20060159563A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; TIPLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53629)B
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                                                                                                                       :|| | | | | 462 IDGLKGHAEKHVTDRMMLNAANIFPFNTPTTK 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 VDGOK-----ATNIFPYTAPGTK 18
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Query Match 47.4%; Score 46; DB Best Local Similarity 34.4%; Pred. No. 8; Matches 11; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
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Best Local Similarity 34.4%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Phaseolus vulgaris
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                                                                                             1 VDGQK-----
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US-11-375-095-104
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47.4%; Score 46; DB 7; Length 581;
Best Local Similarity 34.4%; Pred. No. 8;
Matches 11; Conservative 2; Mismatches 5; Indels
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47.4%; Score 46; DB 7; Length 586;
Best Local Similarity 31.2%; Pred. No. 8.1;
Matches 10; Conservative 4; Mismatches 4; Indels
                                                                                                                                                                                                             DB 7; Length 579;
                                                                                                                                                                                                                                                        5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1293, Application US/11330403
Publication No. US20060159563A1
GENERAL INFORMATION:
APPLICANT: Abad, Mark S.
TITLE OF INVENTION: Genes and Uses for Plant Improvement;
FILE REFERENCE: 38-21(53629)B
CURRENT APPLICATION NUMBER: US/11/330,403
CURRENT FILING DATE: 2006-01-12
NUMBER OF SEQ ID NOS: 19250
SEQ ID NO 1293
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Publication No. US20060159563A1
GENERAL INFORMATION:
APPLICANT: AAA, Mark S.
TITLE OF INVENTION: Genes and Uses for Plant Improvement;
FILE REPRENCE: 38-21(55629)B
CURRENT APPLICATION NUMBER: US/11/330,403
CURRENT FILING DATE: 2006-01-12
SEQ ID NOS: 19250
SEQ ID NO 4518
LENGTH: 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: unsure
: LOCATION: (1)..(581)
: OTHER INFORMATION: unsure at all Xaa locations
US-11-330-403-1293
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47.4%; Score 46; DB
Best Local Similarity 34.4%; Pred. No. 8;
Matches 11; Conservative 2; Mismatches
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CURRENT APPLICATION NUMBER: US/11/330,403
CURRENT FILING DATE: 2006-01-12
NUMBER OF SEQ ID NOS: 19250
SEQ ID NO 18232
LENGTH: 579
                                                                                                               TYPE: PRT
ORGANISM: Glycine max
US-11-330-403-18232
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Pred. No. 9.7;
2; Mismatches 5; Indels 15
RESULT 11
US-11-330-403-7358

US-11-330-403-7358

Sequence 7358, Application US/11330403

Publication No. US20660159563A1

GENERAL INFORMATION:

TITLE OF INVENTION:

FILE REFERENCE: 38-21(53629)B

CURRENT APPLICATION NUMBER: US/11/330,403

CURRENT PILING DATE: 2006-01-12

NUMBER OF SEQ ID NOS: 19250

SEQ ID NO 7358
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Pred. No. 1.1;
0; Mismatches 3
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: I.OCATION: (1)..(581)

: OTHER INFORMATION: unsure at all Xaa locations

US-11-330-403-7358
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US-11-330-403-13229
; Sequence 13229, Application US/11330403
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Publication No. US20060156443A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: YE, JINGSONG
APPLICANT: MENENDEZ-HUMARA, JAIME
APPLICANT: YAN, HIM
                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 33.3%;
Matches 11; Conservative
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Best Local Similarity 72.7%;
Matches 8; Conservative
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US-11-375-095-104
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US-11-330-403-5521
; Sequence 5521, Application US/11330403
; Publication No. US20060159563A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.;
; TILE OP INVENTION:
; FILE REFERENCE: 38-21(53629)B
; CURRENT APPLICATION NUMBER: US/11/330,403
; NUMBER OF SEQ ID NOS: 19250
; SRQ ID NO 5521
; LENGTH: 584
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46.7%; Pred. No. 18;
tive. 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                           Query Match 46.4%; Score 45; DB 7; Length 583; Best Local Similarity 34.4%; Pred. No. 12; Matches 11; Conservative 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 19971, Application US/11330403
Publication No. US20060159563A1
GENERAL INFORMATION:
APPLICANT: Abad, Mark S.
TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REPREBRICE: 38-21 (53629) B
CURRENT APPLICATION UWBER: US/11/330,403
CURRENT APPLICATION NUMBER: US/11/330,403
CURRENT FILING DATE: 2006-01-12
SEQ ID NOS: 19250
LENGTH: 583
Publication No. US20060159563A1
GENERAL INFORMATION:
APPLICANT: Abad, Mark S.
TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REFERENCE: 38-21(53629)B
CURRENT APPLICATION NUMBER: US/11/330,403
CURRENT FILING DATE: 2006-01-12
NUMBER OF SEQ ID NOS: 19250
SEQ ID NO 13229
LENGTH: 583
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; ORGANISM: Securigera parviflora
US-11-330-403-13229
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479 RNAANIYPHNTPSTK 493
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; ORGANISM: Astragalus sinicus
US-11-330-403-5521
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Best Local Similarity 46.7%;
Matches 7; Conservative.
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US-11-330-403-14971
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US-11-330-403-14971
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Search completed: August 30, 2006, 04:35:57 Job time: 10.2727 secs

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August 30, 2006, 04:15:52; Search time 65.4545 Seconds (without alignments) 125.735 Million cell updates/sec
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Biocceleration Ltd.
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GenCore version
Copyright (c) 1993 - 2006
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Maximum Match 100%
Listing first 45 summaries
                                                             OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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geneseqp2003as:*
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geneseqp2000s:*
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length: 200000000
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Maximum DB seq
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Adr10610 Cat IgE e	Adg73237 Cat immun	Abp96580 Cat IgE h	Feli	Abu09336 Feline Ig	Adg73251 Cat parti	5 Cat	9 Dog		_	Aar97753 Canine Ig	Abp96583 Dog IgE h	_	Aab06204 Platypus	Adf90022 Opossum-r	Adn00643 ORO prote	Adf90025 Opossum-h	Adn00646 OSO prote	Aab06206 Immunogen	Aab03644 Opossum I	Aab06208 Immunogen	Aab06205 Immunogen	Aab06207 Immunogen
SUMMARIES	1D	ADR10610	ADG73237	ABP96580	ABU09338	ABU09336	ADG73251	ADG73225	ADR10609	AAY79995	AAW23067	AAR97753	ABP96583	ABP96584	AAB06204	ADF90022	ADN00643	ADF90025	ADN00646	AAB06206	AAB03644	AAB06208	AAB06205	AAB06207
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& Query	March	100.0	100.0	100.0	100.0	100.0	100.0	100.0	89.7	89.7	89.7	89.7	89.7	79.4	74.2	•	61.9			61.9	61.9	61.9	61.9	61.9
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	ADP5588 F19 19E n Aay83167 PGE1 pol Adg42685 Human PAG Adj55754 Peptide h
ADF90033 ADN00651 ADN00661 ABP06591 ABF96591 ADF90027 ADF90035 ADF90035 ADF90035 ADF90037 ADF90029 ADF90029 ADF0012 ADN00650 ADN00650 ADN00650 ADN00650	ABF96588 AAY83167 ADG42685 ADJ55754
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ALIGNMENTS

RESULT 1 ADR10610

Novel antibody that specifically binds to mammalian IgE epitope, useful for testing an allergen reactivity of IgE sample, detecting mammalian IgE or treating asthma or anaphylactic shock. Antiasthmatic; Antiallergic; Immunosuppressive; IgE; dog; asthma; anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody; Cat IgE epitope recognised by monoclonal antibody 3.76, SEQ ID 10. ADR10610 standard; peptide; 18 AA. (UYNC-) UNIV NORTH CAROLINA STATE. 15-JAN-2004; 2004WO-US003566. 16-JAN-2003; 2003US-0440472P. 21-OCT-2004 (first entry) WPI; 2004-593545/57. WO2004065936-A2. Hammerberg B; Felis catus. 05-AUG-2004. ADR10610;

Example 6; Page 9; 14pp; English.

specifically binds to a mammalian IgE epitope, where the epitope is between amino acids 145-166 or 356-374 of mammalian IgE, e.g. dog IgE. (I) is useful for testing an allergen reactivity of an IgE sample. The allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut and corn allergens. The sample is a biological sample collected from a dog, cat or horse. (I) is also useful for detecting mammalian IgE and for treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal antibodies recognise epitopes on canine IgE corresponding to amino acid residues 357-371 (ADR10601) and 146-162 (ADR10609) respectively of the present invention relates to a novel monoclonal antibody (I) that The

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4BP96580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention describes an isolated nucleic acid molecule (I) encoding a portion of a feline IgE heavy chain protein. The methods and compositions of the present invention are useful for eliciting feline immune responses for and/or treating IGE-mediated responses, such as allergies. This is the amino acid sequence of a cat immunoglobulin E (IgE) constant region.
canine IgE epsilon-chain. Recognition of epsilon-chains from IgE from cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and 3.76 were observed to have good cross-reactivity with the epsilon-chain of IgE from cat and horse, but did not exhibit cross-reactivity with either pig or human epsilon-chains of IgE. The present sequence is the cat IgE 3.76 recognition site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic acid molecule encoding a portion of a feline IgE heavy chain protein, useful for treating and/or eliciting feline immune responses for IGE-mediated responses, such as allergies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antiallergic; IgE-modulator; vaccine; feline; IgE; immunoglobulin E; immune response; IgE-mediated response; allergy; cat; constant region.
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                                                                                                                                                    100.0%; Score 97; DB 8; Length 18; 100.0%; Pred. No. 5.7e-09; ive 0; Mismatches 0; Indels
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Pred. No. 1.6e-07;
Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                         Cat immunoglobulin E (IgE) constant region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 12; SEQ ID NO 14; 44pp; English
                                                                                                                                                                                                                                                                                                                                        ADG73237 standard; protein; 431 AA
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Best Local Similarity 100.0%;
Matches 18; Conservative (
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Best Local Similarity 100.
Matches 18; Conservative
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                                                                                                                       Sequence 18 AA;
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emicr. 1. use use to the propose to naturally processed and presented 19E peptides. C1-3 have antiallergic, antiasthmatic, immunosuppressive, vasotropic, dermatological, antialfammatory and cytostatic activities, and can be used as inducers of a CTL response against 1gE, and in vaccines. C1-3 can be used for modulating an IgE-mediated condition in a mammal. C1-3 are useful for modulating an IgE-mediated condition such as IgE-mediated atopic hypersensitivity condition, IgE-mediated non-atopic hypersensitivity condition, IgE-mediated non-atopic hypersensitivity condition, igE myeloma in a mammal. Preferably, C1-3 are useful for treating atopic hypersensitivity conditions (such as allergic athinitis, allergic asthma, food allergies, or atopic dermatitis), non-atopic hypersensitivity conditions (such as anaphylaxis, and urticaria hives). The present sequence represents an IgE heavy chain amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes a method (M1) for identifying peptides that induce cytotoxic T-lymphocyte (CTL) response against immunoglobulin E (IgE), comprising providing a test peptide (T) suspected of being able to bind to major histocompatibility complex (MHC) class I molecule, and naturally processed and presented IgE peptides, where a peptide that induces such a response is identified. Also described are compositions: (C1) comprising at least one immunogenic peptide (I) identified by (M1); (C2) comprising at least one isolated polynucleotide encoding (I); and (I) and (C3) comprising antigen-presenting cells that recognise at least one where C13 are able to bind to at least one MMC class I molecule and to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identifying peptides that induce cytotoxic T-lymphocyte, CTL response against IgE, by identifying peptide eliciting CTL response to IgE peptides naturally presented by major histocompatibility complex class I
                                                                                                                                                                              Immunoglobulin B; vaccine; IgE; cytotoxic T lymphocyte response; immune response; major histocompatibility complex; MHC; immunogenic; antiallergic; antiaethmatic; immunosuppressive; vasotropic; cytostatic; dermatoological; antiinflammatory; IgE-mediated condition; food allergy; atopic hypersensitivity condition; allergic rhintis; allergic asthma; atopic dermatitis; non-atopic hypersensitivity condition; allergic rhintis; allargic asthma; urticaria hives.
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                                                                                                                                      Cat IgE heavy chain amino acid sequence SEQ ID NO:25.
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ABP96580 standard; protein; 496
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                                                                                          (first entry)
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                                                                                             28-MAY-2003
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                                                 ABP96580;
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151 VDGOKATNIFPYTAPGKO 168

1 VDGQKATNIFPYTAPGKQ 18

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100.0%; Score 97; DB 6; Length 496; 100.0%; Pred. No. 1.8e-07;

us-10-758-165a-10.rag

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New nucleic acid molecule encoding feline immunoglobulin E (IgE) heavy or light chain protein, useful for treating feline IgE-mediated responses e.g. allergies, parasitic infections or neoplasia.
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      IgE-mediated immune response; allergy; neoplasia; vaccine technology; antibody technology; antiallergic; antiparasitic; cytostatic.
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                                                                                                                                                                                                         sequence is given as SEQ ID No:14 and claimed in Claim 12"
                                                                                                                                                                                                                                                                                               ID No:11 and
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claimed in Claim 9"
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                                                                                                                                                  Location/Qualifiers
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N-PSDB; ABX95713.
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ses 18; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (WEBE/) WEBER E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid molecule encoding feline immunoglobulin B (IgB) heavy or light chain protein, useful for treating feline IgB-mediated responses e.g. allergies, parasitic infections or neoplasia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to the isolation of feline immunoglobulin E (IgB) kappa light chain and IgE epsilon heavy chain proteins, and the polynucleotide sequences encoding them. The sequences of the invention are useful for treating feline IgB-mediated immune responses (e.g. allergies, parasitic infections or neoplasia), in vaccine technology, sallergical techniques related to feline IgB and its functions the immunological techniques related to feline IgB and its functions. The present sequence represents feline IgB epsilon heavy chain #2
                                                                                                                                                                                                                                                                                                                                                                                                             Feline; immunoglobulin E; IgE epsilon heavy chain; parasitic infection; IgE-mediated immune response; allergy; neoplasia; vaccine technology; antibody technology; antiallergic; antiparasitic; cytostatic.
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100.0%; Pred. No. 1.8e-07;
ive 0; Mismatches 0; Indels
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VDGQKATNIFPYTAPGKQ 233
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WPI; 2004-010802/01
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                                                                                                                                                                                                                     New isolated nucleic acid molecule encoding a portion of a feline IgE heavy chain protein, useful for treating and/or eliciting feline immune responses for IGE-mediated responses, such as allergies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antiallergic, IgE-modulator; vaccine; feline; IgE; immunoglobulin E; immune response; IgE-mediated response; allergy; cat; heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 97; DB 8; Length 496; 100.0%; Pred. No. 1.8e-07;
                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cat partial immunoglobulin E (IgE) heavy chain #1
                                                                                                                                                                                                                                                                                                                                                                                                            ;
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                                                                                                                                                                                                                                                                Claim 8; SEQ ID NO 29; 44pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADG73225 standard; protein; 496 AA.
                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                              216 VDGQKATNIFPYTAPGKQ 233
                                                                                                                                                                                                                                                                                                                                                                                                                                1 VDGQKATNIFPYTAPGKQ 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-APR-2003; 2003US-00409772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-JAN-1999; 99US-0115033P.
                                                                                                07-JAN-1999; 99US-0115033P, 07-JAN-2000; 2000US-00479614.
                                                                           07-APR-2003; 2003US-00409772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                      WPI; 2004-010802/01.
                                                                                                                                                               Mccall C, Weber E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MCCA/) MCCALL C. (WEBE/) WEBER E.
                                                                                                                               (MCCA/) MCCALL C. (WEBE/) WEBER E.
                                                                                                                                                                                                 N-PSDB; ADG73250
                                                                                                                                                                                                                                                                                                                                                                  Sequence 496 AA;
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                                US2003216565-A1
                                                                                                                                                                                                                                                                                               portion of a of the presen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Felis catus
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             Felis catus
                                                       20-NOV-2003
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Weber E;

Mccall C,

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                                                                                                                                                                          The invention describes an isolated nucleic acid molecule (I) encoding a portion of a feline IgE heavy chain protein. The methods and compositions of the present invention are useful for eliciting feline immune responses for and/or treating IGE-mediated responses, such as allergies. This is the amino acid sequence of a partial cat immunoglobulin E (IgE) heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel antibody that specifically binds to mammalian IgE epitope, useful for testing an allergen reactivity of IgE sample, detecting mammalian IgE or treating asthma or anaphylactic shock.
                                        New isolated nucleic acid molecule encoding a portion of a feline IgE heavy chain protein, useful for treating and/or eliciting feline immune responses for IGE-mediated responses, such as allergies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antiasthmatic; Antiallergic; Immunosuppressive; IgE; dog; asthma; anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to a novel monoclonal antibody (I) that
                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dog IgE epitope recognised by monoclonal antibody 3.76, SEQ ID 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                 .
0
                                                                                                                                                                                                                                                                                                                                                                                     Length 496;
                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 97; DB 8; L
100.0%; Pred. No. 1.8e-07;
iive 0; Mismatches 0;
                                                                                                                                    Claim 8; SEQ ID NO 2; 44pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 6; Page 9; 14pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VDGQKATNIFPYTAPGKQ 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADR10609 standard; peptide; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 VDGQKATNIFPYTAPGKQ 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JAN-2004; 2004WO-US003566.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-JAN-2003; 2003US-0440472P.
                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2004-593545/57.
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Les 18; Conserv
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N-PSDB; ADG73224
                                                                                                                                                                                                                                                                                                                                          Sequence 496 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-OCT-2004
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Pred. No. 5.4e-06; Mismatches

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                                                                                                                                                                  ö
cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and 3.76 were observed to have good cross-reactivity with the epsilon-chain of IgE from cat and horse, but did not exhibit cross-reactivity with either pig or human epsilon-chains of IgE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      maximize cross-reactivity to the natural target. They induce safe (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino acid sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen; immunoglopatic; immunoglimulatory; carrier protein; helper T cell epitope; antibody; allergy; allergic disease; immunisation; anti-allergic; anti-asthmatic; asthma; anaphylaxis; dermatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the CH3 domain of immunoglobulin E, fusions
                                                                                                                                                                  Gaps
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                                                                                                                                Length 18;
                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              Dog immunoglobulin E epsilon heavy chain SEQ ID NO:2.
                                                                                                                           Score 87; DB 8; Le
Pred. No. 2.7e-07;
                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 66-68; 155pp; English.
                                                                                                                                                                                                                                                                                                                                  AAY79995 standard; protein; 312 AA
                                                                                                               89.7%; Scur
100.0%; Pre
0; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antigenic peptide from the CF immunization against allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UNBI-) UNITED BIOMEDICAL INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98US-00100287.
                                                                                                                                                                                                      1 VDGQKATNIFPYTAPG 16
                                                                                                                                                                                                                         1 VDGQKATNIFPYTAPG 16
                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wang CY, Walfield AM;
                                                                                                          Query Match
Best Local Similarity
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                                                                                          Sequence 18 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Canis sp.
                                                                                                                                                                                                                                                                                                                                                                    AAY79995;
                                                                                                                                                                                                                                                                                                                 RESULT 9
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89.7%; Score 87; DB 3; Length 312;

Query Match

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This polypeptide is encoded by exons 1-4 (see AAT79278) of canine IgE heavy chain constant region (epsilon) genomic DNA. Another polypeptide, comprising the exon 5 and 6 product, is given in AAW33068. Recombinant peptides encoded by exons 1-6 can be produced in eukaryotic or prokaryotic cells. Such peptides, and antibodies raised against them, are used in methods to treat the manifestation of allergy in dogs, e.g. to treat Type I immediate hypersensitivity, and for immunomodulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated canine IgE heavy chain constant region DNA - useful to develop products for treatment of canine allergies and for immunomodulation in
                                                                                                                                                                                                                                                IgE; immunoglobulin; antibody; heavy chain constant region; allergy;
                                                                                                                                                                                                                                                            hypersensitivity; therapy; dog; antisense; immunomodulation
                                                                                                                                                                                                                        Canine IgE heavy chain constant region (exon 1-4 product).
                                                                                                                                                                                                                                                                                                                                        /note= "encoded by ACC"
                                                                                                                                                                                                                                                                                                                                                                                           'note= "encoded by GCC"
                                                                                                                                                                                                                                                                                                                                                                                                                                             'note= "encoded by GGN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "encoded by TGN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "encoded by GAC"
                                                                                                                                                                                                                                                                                                                                                                                                                   'note= "encoded by NNT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       by NNG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note= "encoded by TCC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 35-39; 59pp; English.
                                                                                                                                                                                                                                                                                                           Location/Qualifiers
55
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                                                                                                                 AAW23067 standard; protein; 417 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97WO-US002322.
                                                                                                                                                                   (revised)
(revised)
(first entry)
                                             VDGQKATNIFPYTAPG
                            1 VDGQKATNIFPYTAPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (IDEX-) IDEXX LAB INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mermer B, Harris RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1997-425031/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference 176
                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference 204
                                                                                                                                                                                                                                                                                                                                                     Misc-difference 56
                                                                                                                                                                                                                                                                                                                                                                             Misc-difference 67
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                                                                                                                                                                                                                                                                                      Canis familiaris.
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16-JUN-2005
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                                                                                                                                                                                             19-FEB-1998
                                                                                                                                           AAW23067;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dogs.
                                                                                          RESULT 10
                                                                                                     AAW23067
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chain amino acid sequence SEQ ID NO:28.

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Identifying peptides that induce cytotoxic T-lymphocyte, CTL response against IgE, by identifying peptide eliciting CTL response to IgE peptides naturally presented by major histocompatibility complex class I
                                                                            Immunoglobulin E, vaccine, IgE; cytotoxic T lymphocyte response; immune response; major histocompatibility complex; MHC; immunogenic; antiallergic; antiaethmatic; immunosuppressive; vasotropic; cytostatic; dermatological; antiinflammatory; IgE-mediated condition; food allergy; atopic hypersensitivity condition; allergic rhinitis; allergic asthma; atopic dermatitis; non-atopic hypersensitivity condition; anaphylaxis;
                                                                                                                                                                                                                                                                                                                                                                                                                      Example 7; Page 152-154; 187pp; English.
                                                                                                                                                                                                                                                                                                                Yang Y, Barankiewicz
                                                                                                                                                                                                                                            08-AUG-2002; 2002WO-US026986.
                                                                                                                                                                                                                                                                   13-AUG-2001; 2001US-0312120P.
                                                                                                                                                                                                                                                                                           (IGET-) IGE THERAPEUTICS INC.
                                (first entry)
                                                                                                                                                                                                                                                                                                                                     WPI; 2003-268242/26.
                                                                                                                                                                        Canis familiaris.
                                                                                                                                                    urticaria hives.
                                                                                                                                                                                               WO2003015716-A2
                                                      Dog IgE heavy
                                28-MAY-2003
          ABP96583;
                                                                                                                                                                                                                                                                                                                Chen SA,
                                                                                                                                                                                                                                                                                                                                                                                                 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The canine IgE amino acid sequence (AAR97753) was deduced from an isolated gene (AAT29824) obtd. from a canine liver DNA library. The cloning of the IgE gene allows produ. of large quantities of recombinant IgE using bacterial, yeast, mammalian, insect or vixal systems. The IgE can be used in drug development (e.g. small molecule screening, assay development and anti-IgE antibody generation). Fragments of IgE can be used in vaccines or to prevent IgE-mediated hypersensitivity. The new sequence information permits targeted modulation of IgE-mediated immune
                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA encoding canine IgE and IgA - useful in vaccines, anti-sense rapy, assays, drug screening, etc.
                                                                                                                                                                                                                                                                                 IgE; immunoglobulin; antibody; vaccine; allergy; hypersensitivity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 426;
                                                          Length 417;
                                                                                0; Indels
            Revised record issued on 30-JUN-2005 : Typo in comments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; Le
                                                         Score 87; DB 2; Le
Pred. No. 7.3e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 87; DB 2; Pred. No. 7.5e 0; Mismatches
                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 11; Page 29-30; 49pp; English.
                                                                                                                                                                                      AAR97753 standard; protein; 426 AA
                                                89.7%; Sc.__
100.0%; Pred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89.7%; Sco.
100.0%; Pre
                                                                                                                           141 VDGQKATNÍFPYTAPG 156
                                                                                                                                                                                                                                                                                                                                                                            95WO-US013795
                                                                                                                                                                                                                                                                                                                                                                                                 94US-00336583.
                                                                                                       1 VDGQKATNIFPYTAPG 16
                                                                                                                                                                                                                                    (first entry)
                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    (MERI ) MERCK & CO INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hollis GF, Patel MD;
                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1996-277321/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
nes 16; Conserv
                                                                                                                                                                                                                                                                                                        Canis familiaris.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                therapy, assays,
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                                   Sequence 417 AA;
                                                                                                                                                                                                                                                                                                                                                                            03-NOV-1995;
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                                                                                                                                                                                                                                                                                                                               WO9614867-A1
                                                                                                                                                                                                                                    28-AUG-1996
                                                                                                                                                                                                                                                                                                                                                     23-MAY-1996
                                                                                                                                                                                                                                                           Canine IgE
                                                                                                                                                                                                             AAR97753;
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The present invention describes a method (M1) for identifying peptides that induce cytotoxic T-lymphocyte (CTL) response against immunoglobulin to Igas, comprising providing a test peptide (T) suspected of being able to bind to major histocompatibility complex (MHC) class I molecule, and naturally processed and presented IgB peptides, where a peptide that induces such a response is identified. Also described are compositions: (C1) comprising at least one immunogenic peptide (I) identified by (M1); (C2) comprising at least one isolated polymuleotide encoding (I); and (C3) comprising antigen-presenting cells that recognise at least one (M) where C1-3 are able to bind to at least one MHC class I molecule and to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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100.0%; Pred. No. 7.5e-06;
iive 0; Mismatches 0;
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100.08; Fr.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 VDGQKATNIFPYTAPG 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 426 AA;
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RESULT 12 ABP96583 ID ABP96583 standard; protein; 426 AA.

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1 VDGQKATNIFPYTAPG

Conservative

Matches

1 VDGQKATNIFPYTAPGKQ 18

295 VDGQKAENLFPYTAPPKR

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the present interaction describes a mercial transportation of the present information describes a mercial transportation of the present information of the providing a test peptide (T) suspected of being able to bind to major histocompatibility complex (MrC) class I molecule, and evaluating (T) for ability to elicit in a mammal a CTL response to naturally processed and presented IgB peptides, where a peptide that induces such a response is identified. Also described are compositions: (C) comprising at least one immunogenic peptide (I) identified by (MI); (C2) comprising at least one isolated polynucleotide encoding (I); and (C) comprising at least one isolated polynucleotide encoding (I); and (C) comprising at least one isolated polynucleotide encoding (I); and (C) are able to bind to at least one MHC class I molecule and to elicit in a mammal a CTL response to naturally processed and presented IS where C1-3 are babe to bind to a natiatilary and cytostatic activities, and can be used as inducers of a CTL response against IgE, and in conformation and can be used as inducers of a CTL response against IgE, and in conformation by a conficient of modulating an IgE-mediated condition in a conformative condition, IgE-mediated condition as the conformation and presential for treating atopic hypersensitivity conditions (such as allergic rhinitis, allergic asthma, food allergies, or atopic dermatitis), non-thine the conformation and the present and the presential and the present and the presential and the presential and the presential and the presential and the presential and the presential and the presential and the presential and the presential and the presential and the presential and the presential and the presential and the presential and the presential and the presential and the presential and the presential and the presential and the presential and the presential and the presential and the presential and the presential and the presential and the presential and the presential and the presential and the presential an
                                                                                                                                                                                                                                                                                                      antiallergic; antiasthmatic; immunosuppressive; vasotropic; cycostatic; dermatological; antiinflammatory; IgB-mediated condition; food allergy; atopic hypersensitivity condition; allergic rhinitis; allergic asthma; atopic dermatitis; non-atopic hypersensitivity condition; anaphylaxis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identifying peptides that induce cytotoxic T-lymphocyte, CTL response against IgE, by identifying peptide eliciting CTL response to IgE peptides naturally presented by major histocompatibility complex class
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes a method (M1) for identifying peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hives). The present sequence represents an IgE heavy chain amino acid sequence, which is given in an example from the present invention
                                                                                                                                                                                            Duckbilled platypus IgE heavy chain amino acid sequence SEQ ID NO:29.
                                                                                                                                                                                                                                                    Immunoglobulin B; vaccine; IgE; cytotoxic T lymphocyte response;
immune response; major histocompatibility complex; MHC; immunogenic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chen Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 7; Page 154-157; 187pp; English.
                             ABP96584 standard; protein; 577 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen SA, Yang Y, Barankiewicz T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-AUG-2002; 2002WO-US026986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-AUG-2001; 2001US-0312120P.
                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (IGET-) IGE THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ornithorhynchus anatinus.
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                                                                                                                                                                                                                                                                                                                                                                                                                            urticaria hives
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-FEB-2003.
                                                                                                                                    28-MAY-2003
                                                                                  ABP96584;
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ABP96584
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Platypus; immunoglobulin E; IgE; vaccination; infection; allergy; asthma; eczema; immunogenic peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chain constant regions 2, 3 and 4 of the platypus IgE. It was used to construct a number of immunogenic peptides which consisted of regions of IgE from different mammals, which appear to cause a stronger polyclonal anti-self IgE response than peptides consisting of the same regions from one mammal. Immunogenic peptides, particularly those consisting of humans, against bacterial and viral infections and allergies, such as asthma, fur, pollen and food allergies and eczema
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     present sequence is an immunogenic peptide consisting of the heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunogenic polypeptides useful for preventing the harmful effects of immunoglobulin E in mammals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74.2%; Score 72; DB 3; Length 343; ilarity 72.2%; Pred. No. 0.002; Conservative 3; Mismatches 2; Indels
                                                                                          Platypus IgE heavy chain constant regions 2, 3 and 4.
                                                                                                                                                                                                                         /note= "Xaa=unknown"
                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADF90022 standard; protein; 337 AA.
            AAB06204 standard; protein; 343 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 2; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 VDGQKATNIFPYTAPGKQ 18
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                                                                                                                                                                                              Misc-difference 1. .343 /label OTHER
                                                                                                                                                                                                                                                                                                                                   98US-0106652P
                                                                                                                                                                                                                                                                                                                                                                      (RESI-) RESISTENTIA PHARM AB
                                                                                                                                                                                                                                                                                                                                              99US-00401636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 VDGQKAEHLFPYTAPPKR
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                                                             22-NOV-2000 (first entry)
                                                                                                                                                         Ornithorhynchus anatinus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
see 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 343 AA;
                                                                                                                                                                                                                                                   WO200025722-A2
                                                                                                                                                                                                                                                                                                                                 02-NOV-1998;
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                                                                                                                                                                                                                                                                             11-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                  Hellman LT;
                                       AAB06204;
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Matches
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ADF90022
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79.4%; Score 77; DB 6; Length 577; 77.8%; Pred. No. 0.00049; ive 2; Mismatches 2; Indels

Query Match 17.8 Best Local Similarity 77.8 Matches 14; Conservative

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The present sequence is the protein sequence of an opossum CH2-rat CH3-opossum CH4 (ORO) chimeric IgE polypeptide. A vector comprising a nucleic acid encoding ORO can be used for recombinant production of this chimeric IgE in host, e.g. CHO, cells. The invention provides methods and materials related to expressing chimeric IgE proteins. Nucleic acid vectors, host cells, and methods for producing chimeric IgE polypeptides are provided. When administered to a mammal, the chimeric polypeptides can reduce the IgE antibody effects of IgE-related diseases such as asthma, allergies and eczema.
                                                                                                                                                                                                                                                                                                                                                                                                                             New host cell comprising a nucleic acid vector comprising a cytomegalovirus promoter, an Ig leader sequence, an insert sequence or SV40 late polyadenylation sequence, useful in producing a chimeric IgE polypeptide.
                                            IgE; immunoglobulin; antibody; opossum; rat; vaccine; antiallergic; antiasthmatic; dermatological.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
61.9%; Score 60; DB 8; Length 337;
Best Local Similarity 61.1%; Pred. No. 0.2;
Matches 11; Conservative 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                              Magnusson A;
                Opossum-rat chimeric IgE polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 3; SEQ ID NO 3; 23pp; English.
                                                                                                                                                                                                                                         15-MAY-2003; 2003WO-IB002503.
                                                                                                                                                                                                                                                                            21-MAY-2002; 2002US-0382552P
                                                                                                                                                                                                                                                                                                            (RESI-) RESISTENTIA PHARM AB.
                                                                                                                                                                                                                                                                                                                                                                                WPI; 2004-042496/04.
N-PSDB; ADF90020, ADF90021.
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                                                                                                  Chimeric.
Didelphis virginiana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 337 AA;
                                                                                                                                                                     WO2003096966-A2
                                                                                                                                                                                                                                                                                                                                              Lundgren M,
                                                                                                                                                                                                       27-NOV-2003
                                                                                                                                      Rattus sp.
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Gaps

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Search completed: August 30, 2006, 04:22:05 Job time : 66.4545 secs

1 VDGQKATNIFPYTAPGKQ 18 VDGQEAENLFPYTTRPKR 73

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

August 30, 2006, 04:29:42; Search time 10.7273 Seconds (without alignments) 161.448 Million cell updates/sec Run on:

US-10-758-165A-10

1 VDGQKATNIFPYTAPGKQ 18 Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 Total number of hits satisfying chosen parameters:

283416 segs, 96216763 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	hypothetical prote		probable surface p	41	El protein - human	conserved hypothet	hypothetical prote	conserved hypothet	hypothetical prote	protein F54D8.3 [i	hypothetical prote	NADPH-cytochrome P	hypothetical prote	DNA primase XF2025	DNA primase XF2061	conserved hypothet	hypothetical prote	conserved hypothet	conserved hypothet	serine proteinase	licheninase (EC 3.	puative trans-acon	hypothetical prote	probable polyamine	hypothetical prote	spermidine/putresc	conserved hypothet	BH0982 hypothetica	probable squalene
SUMMAKIES	ΙD	T16880	S62057	AH0110	AD2436	S15623	B71325	S74487	A87692	T17798	D88449	T22177	JE0230	T49648	C82607	D82606	G69203	F89886	D90167	C75582	C89967	LXBS	AF0306	S40753	G81926	T32714	C81179	AH2821	H97599	T07942
	DB	2	~	7	7	Н	7	7	7	~	7	7	~	7	~	7	~	~	~	~	7	н	~	~	~	~	7	7	7	0
	Length	270	633	658	381	643	683	1032	1686	241	544	623	713	2298	363	1371	101	109	179	227	240	242	258	327	374	391	419	454	470	206
٠	Query Match	49.5	44.3	44.3	43.3	43.3	43.3	43.3	43.3	42.3	42.3	42.3	42.3	42.3	41.8	41.8	41.2	41.2	41.2	41.2	41.2	41.2	41.2	41.2	41.2	41.2	41.2	41.2	41.2	41.2
	Score	48	43	43	42	42	42	42	42	41	41	41	41	41	40.5	40.5	40	40	40	40	40	40	40	40	40	40	40	40	40	40
	Result No.	1	8	٣	4	Ŋ	9	7	80	D	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

hypothetical prote phosphatidylinosit	coat protein gamma glycoprotein B - h hypothetical prote	probable outer mem isoleucyl-trna syn hypothetical prote	fatty-acid synthas fatty acid synthas transcription elon	hypotherical prote hypothetical prote hypothetical prote T6J4.7 protein - A
T16078 T07745 T07761	10//01 T05265 QQBELL T12526	G71460 T40751 T28895	H70656 A87058 A69637	C64041 H95965 F95416 G86267
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645 812 814	831 831 857 915	1013 1064 1203	3069 3076 157	213 308 308 374
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30 31	3 8 8 8 3 8 4 8	36 37 38	39 4 4 0 11	44 44 44 ርርርር 44 72

ALIGNMENTS

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A,Accession: T16880
A,Status: preliminary: translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Residues: 1-270 <WIL>A,Residues: 1-270 <WIL>A,Residues: UAID: UNIPARC: UPI0000075025; EMBL: U41268; NID: g1086843; PI
                                                                                          C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 05-Oct-2004 C;Accession: T16880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: CESP:T14G12.4
A;Introns: 37/1; 72/3; 164/1
F;93-185/Domain: fork head DNA-binding domain homology <FHD>
                                                                                                                                                                   Riwilcox, L. submitted to the EMBL Data Library, November 1995 A;Description: The sequence of C. elegans cosmid T14G12. A;Reference number: Z18596
I16880
hypothetical protein T14G12.4 - Caenorhabditis elegans
                                                                     C; Species: Caenorhabditis elegans
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Gaps .; 0 Length 270; 4; Indels Query Match
49.5%; Score 48; DB 2;
Best Local Similarity 57.1%; Pred. No. 1.8;
Matches 8; Conservative 2; Mismatches

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205 GAAAANLFPYFSPG 218 3 GOKATNIFPYTAPG 16 셤 ઠ

proline-rich protein LAS17 - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein 04724; protein YOR181w
C;Species: Saccharomyces cerevisiae
C;Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
C;Accession: S62057; S67073

when it is to the EMBL Data Library, December 1995
A, Description: Yeast mutants sensitive to local anesthetics.
A, Reference number: \$62057

A;Accession: S62057
A;Adlecule type: DNA
A;Molecule type: DNA
A;Residues: 1-633 «TOH»
A;Cross-references: UNIPROT:Q12446; UNIPARC:UPI000003CA29; EMBL:D78487; NID:g1101756; PI
Sthudhes, B.; Pohl, T.M.
submitted to the Protein Sequence Database, July 1996
A;Reference number: S66685

A; Accession: S67073

A;Molecule type: DNA A;Residues: 1-633 «HUG> A;Cross-references: UNIPARC:UP1000003CA29; EMBL:Z75089; NID:g1420436; PID:e252060; PID:g A;Experimental source: strain S288C

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Gaps

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A; Cross-references: UNIPROT: P22153; UNIPARC: UPI0000138313; EMBL: X55965; NID: g60882; PIDN C; Superfamily: papillomavirus El protein C; Keywords: early protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cyaccession: B71325
RiFraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin. rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDo. trson, J.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A; Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A; Reference number: A71250; MUID: 98332770; PMID: 9665876
A; Reference runder: A1225
A; Reference submay and leic acid sequence not shown; translation not shown
A; Residues: 1-683 <CCL>
A; Residues: 1-683 <CCL>
A; Experimental source: strain Nichol8
A; Experimental source: strain Nichol8
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A;Vaziety. PCC 6803
A;Vaziety. PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S74487
C;Accession: S74487
Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
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                                                                                                                                                                                            C;Accession: S15623
R;Hirsch-Behnam, A.; Delius, H.; de Villiers, E.M.
Virus Res. 18, 81-98, 1990
A;Title: A comparative sequence analysis of two human papillomavirus (HPV) types 2a and A;Reference number: S15614; MUID:91188699; PMID:1964523
A;Accession: S15623
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          conserved hypothetical protein TP0421 - syphilis spirochete
C,Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C,Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
                                                                                                                                  A;Note: host Homo sapiens (man)
C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
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A;Accession: S74487
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 643;
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Pred. No. 51;
3; Mismatches
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3; Mismatches
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                                                             El protein - human papillomavirus type 57
C;Species: human papillomavirus type 57
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ilarity 53.8%;
Conservative 3
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278 GQKSARFFGFSAPG 291
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581 KFTNPFPFASPGE 593
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Best Local Similarity 50.0%
Best Accompanies
To Conservative
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Best Local Similarity
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A,Title: Genome sequence of Yersinia pestis, the causative agent of plague. A,Title: Genome sequence or Wersinia pestis, the causative agent of plague. A,Reference number: AB0001; MUDD:21470413; PMID:11586360
A,Recession: AH0110
A,Status: preliminary
A,Molecule type: DNA
A,Molecule type: DNA
A,Residues: 1-658 <KUR>
A,Conserreferences: UNIPROT:08ZHJO; UNIPARC:UPI0000CD765; GB:AL590842; PIDN:CAC89747.1;
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Pred. No. 29;
1; Mismatches 6; Indels
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61.5%; Pred. No. 35;
                                                                                                                                                                       Length 633;
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3; Mismatches
                                                                                                                                                                       Score 43; DB
Pred. No. 34;
2; Mismatches
                             A;Gene: SGD:LAS17
A;Cross-references: SGD:S0005707; MIPS:YOR181w
A;Map position: 15R
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53.3%;
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53.3%;
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99 LNGQKATNLAPAT 111
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Best Local Similarity 53.33
Matches 8; Conservative
                                                                                                                                          Query Match
Best Local Similarity 53.3°
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Best Local Similarity 61.5
Best Local 8; Conservative
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C, Genetics:
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A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_eleA;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
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R;Yamada, T.; Imaishi, H.; Oka, A.; Ohkawa, H.
Bisci. Biotechnol. Biochem. 62, 1403-1411, 1998
A;Title: Molecular cloning and expression in Saccharomyces cerevisiae of tobacco NADPH-c<sup>.</sup> A;Reference number: JE0230; MUID:98386693; PMID:9720224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Cross-references: UNIPROT:002260; UNIPARC:UPI000017B9C4; EMBL:Z81083; PIDN:CAB03101.1; A,Experimental source: clone F44F1
                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-544 <STO>
A;Cross-references: UNIPROT:Q20780; UNIPARC:UPI0000174F99; GB:chr_III; PIDN:AAA20615.1;
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C,Superfamily: NAD-dependent aldehyde dehydrogenase; aldehyde dehydrogenase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein F44F1.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T22177
      protein F54D8.3 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
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C;Species: Nicotiana tabacum (common tobacco)
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 09-Jul-2004
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A;Introns: 43/2; 69/3; 181/3; 241/2; 493/3; 526/2; 548/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 41; DB 2;
Pred. No. 74;
0; Mismatches
                                                                                                                R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R,Dobson, R. submitted to the EMBL Data Library, October 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12.3%; Score 41; DB larity 44.4%; Pred. No. 63; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     152 VDGQWKTIIIDDYFPYTTDG 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 VDGQKATNI----FPYTAPG 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          389 VDGKQVETILKYIAAGKK 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 VDGQKATNIFPYTAPGKQ 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 55.0%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Reference number: Z19527
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Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-713 <YAM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Residues: 1-623 <WIL>
                                                                                                                                                                                                                                                                                                     A;Accession: D88449
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Gene: CESP: F44F1.3
                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: JE0230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A, Accession: T22177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Gene: F54D8.3
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Conserved hypothetical protein CC3571 [imported] - Caulobacter crescentus

C;Species: Caulobacter crescentus

C;Species: Caulobacter crescentus

C;Accession: A87692

R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. A;Tile: Complete Genome Sequence of Caulobacter crescentus.

A;Title: Complete Genome Sequence of Caulobacter crescentus.

A;Accession: A87692
      GB:AB001339; NID
June 1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:Q9A2J0; UNIPARC:UPI00000C7B14; GB:AE005673; NID:g13425311; C;Genetics:
A;Gene: CC3571
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T17798

hypothetical protein A301L - Chlorella virus PBCV-1

hypothetical protein A301L - Chlorella virus PBCV-1

C;Species: Chlorella virus PBCV-1

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C;Accession: T17798

R;Graves, M.V.; Van Etten, J.L.

Submitted to the EMBL Data, J.L.

A;Reference number: Z18806
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A, Cross-references: UNIPROT: P72637; UNIPARC: UPI0000139F8B; EMBL: D90899; A,NOCE: the nucleotide sequence was submitted to the EMBL Data Library, C;Genetics:
A,Start codon: GTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1686;
                                                                                                                                                  DB 2; Length 1032;
87;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43.3%; Score 42; DB 2; I 66.7%; Pred. No. 1.5e+02; iive 1; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Accession: T17798
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Reaidues: 1-24: <GRA>
                                                                                                                                                                                                                 5; Mismatches
                                                                                                                                                  Query Match 43..3%; Score 42; Best Local Similarity 35.3%; Pred. No. 8 Matches 6; Conservative 5; Mismatch
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732 IDAYTTSNSYPYSDPGE 748
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GOKATTVFPLGA 297
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A;Status: preliminary A;Molecule type: DNA A;Residues: 1-1686 <STO>

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Query Match Best Local Similarity Matches 8; Conserv

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|:|||| | NVFPYTGP 189 8 NIFPYTAP 15

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RESULT 10

Local Similarity

Query Match Best Loca Matches

9

Length 363;

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Search completed: August 30, 2006, 04:30:56 Job time : 11.7273 secs
A;Contents: annotation
C;Genetics:
A;Gene: XF2025
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                                                                                                                                         Query Match
Best Local
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CG2607
Cyspecies X72025 [imported] - Xylella fastidiosa (strain 9550)
Cyspecies: Xylella fastidiosa
Cyspecies: Xylella fastidiosa
Cypate: 18-Aug-2000
#sequence _revision 20-Aug-2000 #text_change 09-Jul-2004
Cypate: 18-Aug-2000
#sequence of the plant pathogen Xylella fastidiosa.
Ryanonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequence of the plant pathogen Xylella fastidiosa.
Ayritte: The genome sequence of the plant pathogen Xylella fastidiosa.
Ayreference number: A02515; MUID:20365717; PMID:10910347
AyNote: for a complete list of authors see reference number A59328 below
Ayreference number: A02515; MUID:20365717; PMID:10910347
Ayreference number: Excapa Pastor Ayreference number A59328 below
Ayreference number: Extrain Pastor
Ayreferences: UNIPROT:Q9PBW0; UNIPARC:UPI00000C28EE; GB:AE004021; GB:AE003849; NID
Ayreferences: UNIPROT:Q9PBW0; UNIPARC:UPI00000C28EE; GB:AE004021; GB:AE003849; NID
Ayreferences: UNIPROT:Q9PBW0; UNIPARC:UPI00000C28EE; GB:AE004021; GB:AE003849; NID
Ayreferences: UNIPROT:Q9PBW0; UNIPARC:UPI00000C28EE; GB:AE004021; GB:AE003849; NID
Ayreferences: UNIPROT:Q9PBW0; UNIPARC:UPI00000C28EE; GB:AE004021; GB:AE003849; NID
Ayreferences: UNIPROT:Q9PBW0; UNIPARC:UPI00000C28EE; GB:AE004021; GB:AE003849; NID
Ayreferences: UNIPROT:QPBW0; UNIPARC:UPI00000C28EE; GB:AE004021; GB:AE003849; NID
Ayreferences: MR.S.; Buenco, MR.P.; Racincani, A.P.; Franca, S.C.; Franco, D.M.; Submitted to GenBank, June 2000
AyAuthors: Ferreira, W.C.A.; Ferraica, A.M.; Marxins, E.A.; Authors: Madeira, A.M.B.M.; Madeira, M.M.; Madeira, M.M.; Madeira, A.M.; M.B.; Madeira, A.M.; Madeira, A.M.; Madeira, A.M.; Madeira, A.M.; Madeira, A.M.; Madeira, A.M.; Madeira, A.M.; Madeira, A.M.; Madeira, A.M.; Madeira, A.M.; Madeira, A.M.; Madeira, A.M.; Madeira, M.J.; Madeira, M.J.; Madeira, M.J.; Madeira, M.J.; Madeira, M.J.; Madeira, M.J.; Madeira, M.J.; Madeira, M.J.; Madeira, M.J.; Madeira, M.J.; Madeira, M.J.; Madeira, M.J.; Madeira, M.J.; Madeira, M.J.; Madeira, M.J.; Madeira, M.J.; Madeira, M.J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Reference number: Z25022
A;Accession: T49648
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-2298 < SCH:
A;Cross-references: UNIPROT:Q96U00; UNIPARC:UPI000017B4BA; EMBL:AL355933; GSPDB:GN00116;
A;Experimental source: BAC clone B8B20; strain OR74A
   C,Superfamily: NADPH-ferrihemoprotein reductase; flavodoxin homology; NADPH-ferrihemoprd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T49648
hypothetical protein B8B20.20 [imported] - Neurospora crassa
C;Species: Neurospora crassa
C;Species: Neurospora crassa
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
C;Accession: T49648
R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, May 2000
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                                        C;Keywords: flavoprotein; oxidoreductase
F;107-712/Domain: NADPH-ferrihemoprotein reductase homology <FEH>
F;109-257/Domain: flavodoxin homology <FLX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42.3%; Score 41; DB 2; Length 2298; 42.9%; Pred. No. 3.1e+02; ive 3; Mismatches 5; Indels
                                                                                                                                                                                     2; Length 713;
                                                                                                                                                                                                                                                           5; Indels
                                                                                                                                                                                     Score 41; DB
Pred. No. 85;
                                                                                                                                                                                                                                                        1; Mismatches
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                                                                                                                                                                                 42.3%;
ilarity 57.1%;
Conservative
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Best Local Similarity
                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 8; Conserv
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A,Gene: NCSP:BBB20.20
A,Map position: 6
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DNA primase XF2061 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: D82606
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequent Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Cross-references: UNIPROT: O9PBS8; UNIPRAC: UFI00000C290E; GB:AE004022; GB:AE003849; NID A,Cross-references: strain 9a5c
R,Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carreira, D.M.; Carrer, H Briones, M.R.S.; Bueno, M.R.P.; Fearincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A,Puthors: Ferreira, V.C.A.; Ferro, J.A.; Frainca, J.S.; Franca, S.C.; Franco, M.C.; Frohmu J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr: chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marsuco, C.L.; Marques, M.V.; Martins, E.A.; Alauthors: Martins, E.M.P.; Matsukuma, A.Y.; Menc, C.C.; Marques, M.V.; Martins, E.G.; Nunes, L.R.; Ollveira, M.A.; de Ollveira, M.C.; de Ollveira, R.C.; Palmieri, D.A.; F.G.; Nunes, L.R.; Ollveira, M.A.; de Ollveira, M.C.; Sawasak, A.Juthors: ad Silva, A.J. de M.; Gelveira, A.M.; Silva Jr., W.A.; da Silvaira, M.A.; da Silvaira, A.M.; Silva Jr., W.A.; da Silvaira, A.R.; Silva Jr., W.A.; da Silvaira, A.R.; Silva Jr., W.A.; da Silvaira, A.R.; Silva Jr., W.A.; da Silvaira, M.A.; Verfore, A.L.; Z.
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Pred. No. 2.2e+02;
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Bacteria; Fusobacteria; Fusobacterales; Fusobacteriaceae;
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Q94b26 oryza sativ
Q512w7 bordetella
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Q21h1 caenorhabdi
Q91ku5 streptomyce
Q41km3 g1bberella
Q22h01 caldicellul
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Distributed under the Creative Commons Attribution-NoDerivs License
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                          MEDLINE-21886394; PubMed=11889109; MEDLINE-21886394; PubMed=11889109; MEDLINE-21886394; PubMed=118892002; Kapatral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A., Bhattacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L., Vasieva O., Chu L., Kogan Y., Chaga O., Goltsman E., Bernal A., Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R., Fonstein M., Kyrpides N.C., Overbeek R.; "Genome sequence and analysis of the oral bacterium Fusobacterium unclearum strain ATCC 25586."; J. Bacteriol. 184:2005-2018(2002).
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MEDLINE=99069613; PubMed=9851916; DOI=10.1126/science.282.5396.2012;
The C. elegans sequencing consortium;
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SMR; 0950A9; 2-68.

Ensembl; T14G12.4; Caenorhabditis elegans.

Mormbase; WBGene00001434; Ekh-2.

MormPep; T14G12.4b; CE29342.

GO; GO:0005534; C:nucleus; IEA.

GO; GO:0000350; F:renucleus; IEA.

GO; GO:000350; P:regulation of transcription, DNA-dependent; IEA.

GO; GO:0005350; P:remacription; IEA.

InterPro; IPR0011991; Wing_hlx_DNA_bd.
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01-DEC-2001, sequence version 1.
07-FRB-2006, entry version 28.
Forkhead transcription factor family protein 2, isoform b.
Name-Ekh-2; ORFNames=T14G12.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE009951; AAL94414.1; -; Genomic_DNA.
BioCyc; FNUC190304:FN0208-MONOMER; -.
GO; GO106829; F:1yase activity; IEA.
InterPro; IPR010327; HGD-D.
Pfam; PF06050; HGD-D.
Complete proteome; Lyase.
SEQUENCE 382 AA; 43923 MW; 93038D4296AE34CD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                      NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U41268; AAL02521.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Science 282:2012-2018(1998).
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28 EGKKAVGIFPYYAP 41
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Best Local Similarity
                              NCBI_TaxID=76856;
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Q95QA9;
       Fusobacterium
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Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Bristol N2;
MEDLINE=99069613; Pubmed=9851916; DOI=10.1126/science.282.5396.2012;
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R WormBase, WEGenco0001434; fkh-2.

R GO, GO:005515; F:protein binding, IPI.

R InterPro; IPR011591; Wing hix bad.

R InterPro; IPR011591; Wing hix bad.

R Pfam; PF00250; Fork head; 1.

R PROSTIF; PR00653; FORKHEAD.

R PROSTIF; PR00653; FORK HEAD 1:

R PROSTIF; PS00659; FORK HEAD 2:

R PROSTIF; PS00659; FORK HEAD 2:

R PROSTIF; PS00659; FORK HEAD 3:

R Complete proteome: DNA-binding; Nuclear protein; Transcription;
PRINTS; PROSSS; FORTHEAD.

PRODOM; PRO00425; TE Fork_head; 1.

PROSTITE; SM00139; FH; 1.

PROSTITE; PS50059; FORK_HEAD 2; 1.

PROSTITE; PS50039; FORK_HEAD 2; 1.

PROSTITE; PS50039; FORK_HEAD 3; 1.

Transcription regulation.

SEQUENCE 168 AA; 19239 MW; BEOLAC4E69968572 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The C. elegans sequencing consortium;
"Genome sequence of the nematode C. elegans: a platform for
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Forkhead transcription factor family protein 2, isoform a.

Name=fkh-2; ORFNames=T14G12.4;
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SEQUENCE 270 AA, 30491 MW, 7C49116E5EC76175 CRC64;
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20;
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49.5%; Score 48; DB
Best Local Similarity 57.1%; Pred. No. 20;
Matches 8; Conservative 2; Mismatches
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HSSP; Q9958; 1D5V.
SMR; Q22510; 93-170.
INTAC; Q22510; --
Ensembl; T14G12.4; Caenorhabditis elegans.
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Science 282:2012-2018(1998).
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103 GAAAANLFPYFSPG 116
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                                                                                                                                                                                                                                                                                             Local Similarity 57.1
nes 8; Conservative
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Detter J.C., Glavina T.,

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Distributed under the Creative Commons Attribution-NoDerivs License
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PubMed=15383840; DOI=10.1371/journal.pbio.0020303;
Ward N.L., Larsen O., Sakwa J., Bruseth L., Khouri H.M., Durkin A.S., Dimitrov G., Jiang L., Scanlan D., Kang K.H., Lewis M.R., Nelson K.E. Methe B.A., Wu M., Heidelberg J.F., Paulsen I.T., Fouts D.E., Ravel J., Tettelin H., Ren Q., Read T.D., DeBoy R.T., Seshadri R., Salzberg S.L., Jensen H.B., Birkeland N.K., Nelson W.C., Dodson R.J., Grindhaug S.H., Holt I.E., Eidhammer I., Jonasen I., Vanaken S., Utterback T.R., Feldblyum T.V., Fraser C.M., Lillehaug J.R.,
                 Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavine Hammon N., Israni S., Pitluck S., Richardson P.; "Sequencing of the draft genome and assembly of Rhodopseudomonas
                                                                                                                                                                                                                                                                                 -!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Methylococcus capsulatus.
Bacteria; Proteobacteria; Gammaproteobacteria; Methylococcales;
Methylococcaceae; Methylococcus.
                                                                                                                                                     STRAIN-BISAS3;
US DOE Joint Genome Institute (JGI-ORNL);
Larimer F., Land M.;
"Annotation of the draft genome of Rhodopseudomonas palustris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48.5%; Score 47; DB 2; Length 365; 50.0%; Pred. No. 42;
                                                                           palustris BisA53.";
Submitted (OCT-2005) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                (OCT-2005) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40239 MW; E11D3C9BC0F1244F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-NOV-2004, sequence version 1.
07-FBB-2006, entry version 9.
Hydrophobe/amphiphile Efflux-1 (HAB1) family protein.
OrderedLocusNames-MCA1360;
                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AALA01000029; EA087857.1; -; Genomic_DNA. Hypothetical protein. SEQUENCE 365 AA; 40239 MW; E11D3C9BC0F1244F
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DOE Joint Genome Institute (JGI-PGF);
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Best Local Similarity 50.v.
8; Conservative
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                                                                                                                                    NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                US DOE Joint Genome Institute (JGI-PGF);
Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T., Hammon N., Israni S., Pitluck S., Richardson P.;
"Sequencing of the draft genome and assembly of Nitrosomonas eutropha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US DOB JOINT Genome Institute (JGI-ORNL);
Larimer F., Land M., Hauser L.;
"Annotation of the draft genome assembly of Nitrosomonas eutropha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
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                                                                                                                                                                                        25-OCT-2005, integrated into UniProtKB/TrEMBL.
25-OCT-2005, sequence version 1.
07-FBB-2006, entry version 3.
Putative type 4 fimbrial biogenesis protein PilY1 precursor.
ORFNames=NeutDRAFT_0559;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Rhodopseudomonas.
NCBI_TaxID=316055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49.5%; Score 48; DB 2; Length 1143; 64.3%; Pred. No. 95;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1143 AA; 123766 MW; 9C270A88F6A0FAF1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                       PRT; 1143 AA.
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07-FBB-2006, entry version 3.
Hypothetical protein.
ORFNames=RPEDRAFT 0215;
                                                                                                                                                                                                                                                                                                                                          Nitrosomonadaceae; Nitrosomonas.
                                                                                                                                                     Q3N7V1_9PROT PRELIMINARY;
                                       GAAAANLFPYFSPG 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DGSKLTNHFPNTSP 396
                 GOKATNIFPYTAPG 16
                                                                                                                                                                                                                                                                                                     Nitrosomonas eutropha C71.
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les 9; Conservative
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STRAIN=BisA53;
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Matches

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036VF1
036VF1
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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                           Kube M., Beck A., Meyerdierks A., Amann R., Reinhardt R., Rabus "A catabolic gene cluster for anaerobic benzoate degradation in methanotrophic microbial Black Sea mats.";
Syst. Appl. Microbial 28:287-294(2005).
- SIMILARITY: Belongs to the thiolase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The genome sequence of the poultry pathogen Bordetella avium, genomic comparisons with related species infecting mammals."; Submitted (NOV-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bordetella avium 197N.
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
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46.9%; Score 45.5; DB 2; Length 491;
Best Local Similarity 47.6%; Pred. No. 1e+02;
Matches 10; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, CR931837; CAI78864.1; -; Genomic_DNA.
InterPro; IPR002155; Thiolase.
PANTHER, PTHR18919; Thiolase; 2.
Pfam; PF02037; Thiolase C; 1.
Pfam; PF02037; Thiolase N; 1.
TIGRFANS; TIGR01930; ACCAA-C-Actrans; 1.
SEQUENCE 408 AA; 43389 \( \text{MW} \); F9BECC546AF32193 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AM167904; CAJ48922.1; -; Genomic DNA.
SEQUENCE 491 Aa; 54500 MW; E900B690162C1AA4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                        PubMed=15997700; DOI=10.1016/j.syapm.2005.02.006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-MAR-2006, integrated into UniProtKB/TrEMBL. 07-MAR-2006, sequence version 1. 07-MAR-2006, entry version 1. Putative phage portal protein.
                                                                             10-MAY-2005, integrated into UniProtKB/TrEMBL.
10-MAY-2005, sequence version 1.
21-FEB-2006, entry version 6.
                        408 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                     PRT;
                                                                                                                                                                                                                                                            Bacteria; environmental samples.
NCBI_TaxID=77133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : | | | | | | 45 IDASIGANVYQFTAPGAQ 62
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                        PRELIMINARY;
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                                                                                                                                                                           3-oxoacyl-CoA thiolase.
                                                                                                                                                                                                                                      uncultured bacterium
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                        Q565U8_9BACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP clade;
Ehrhartoideae, Oryzeae, Oryza.
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                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Buell C.R., Yuan Q., Ouyang S., Moffat K.S., Hill J.N., Gansberger Bernner M., Burgeses S., Hance M., Shvatebeyn M., Taltrin T., Riggs F., Hsiao J., Zismann V., Blunt S., Pai G., Vanken S.E., Utterback T.R., Feldblyum T.V., Quackenbush J., Salzberg S.L., Mitte O., Fraser C.M., "Or, Quackenbush J., Salzberg S.L., "Oryza sativa chromosome 3 BAC OSJNBa0077G22 genomic sequence."; Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
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Pred. No. 1.9e+02;
2; Mismatches 3; Indels
                                                                                                                                                                           48.5%; Score 47; DB 2; Length 1054; 56.2%; Pred. No. 1.3e+02; ive 2; Mismatches 5; Indels
                                                                                                                   1054 AA; 115005 MW; BB032CB91B38D1A8 CRC64;
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Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
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GG; G01000367; F:DNA binding; IEA.
GO; G0:0004523; F:Tibonuclease H activity; IEA.
GO; GO:0015074; P:DNA integration; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-2001, integrated into UniProtKB/TrEMBL. 01-DEC-2001, sequence version 1. 21-FEB-2006, entry version 18.
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PROSITE; PS50879; RNASE_H; 1.
                            PRINTS; PR00702; ACRIFLAVINRP.
TIGREAMS; TIGR00915; 2A0602; 1.
                                                                                                                                                                                                                                                                                                                                                                294 VNGHKSTQIVVYTLPG 309
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Name=OSJNBa0077G22.13;
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Similarity 61.5%;
8; Conservative
      Pfam; PF00873; ACR tran; 1.
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740 VDGRAAVNLMPYT 752
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                                                                                                                                                  Query Match
Best Local Similarity 56.2

Local 9; Conservative
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Best Local Similarity
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                                                                                       Complete proteome
SEQUENCE 1054 A
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Q94H26;
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SEQUENCE
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Length 408; Indels

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3 GOKATNIF-----PYTAPG 16

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Matches

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    -!- COFACTOR: Zinc (By similarity).
    -!- PATHWAY: Degradation of allantoin (purine catabolism); first step.
    -!- SIMILARITY: Belongs to the DHOase family.

                                                                                                                                                                                                         MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a; Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L., Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H., Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M., Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S., Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neil S., Rabbinowitsch E., Rajandream M.A., Rutherford K.M., Rutter S., Seeger K., Saunders D., Sharp S., Squares S., Taylor K., Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam, PF01979; Amidohydro_1; 1.
ProDom; PD000518; DH0base; 1.
Complete proteome, Hydrolase; Hypothetical protein; Metal-binding;
Purine metabolism; Zinc.
                                                                                                                                                                                                                                                                                                                                                                                                                                            "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";
Nature 417:141-147(2002).
-!- CATALYTIC ACTIVITY: (S)-allantoin + H(2)O = allantoate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein.

ORFNames=FG03975.1;

GREDSPFELLa zeae (Fusarium graminearum).

Eukaryota; Fungi; Ascomycota; Perizomycotina; Sordariomycetes; Hypocreales; Nectriaceae; Gibberella.

NCBI_TaxID=5518;
                                                                                        Streptomyces coelicolor.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46:4%; Score 45; DB 1; Length 445;
                        07-MAR-2006, entry version 37.
Probable allantoinase (EC 3.5.2.5).
OrderedLocusNames-SCO6247; ORFNames=SCAH10.12, STAH10.12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75955C5F98632570 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Probable allantoinase.
/FIId=PRO 0000165943.
Zinc (Potential).
Zinc (Potential).
                                                                                                                     Streptomycineae, Streptomycetaceae; Streptomyces
NCBI_TaxID=1902;
                                                                                                                                                                                        NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-AUG-2005, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        811 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AL939126; CAB60166.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GenomeReviews; AL645882 GR; SCO6247.
BioCyc; SCOB1902:SCO6247-MONOMER; -.
InterPro; IPR006680; Amidohydro_1.
InterPro; IPR005847; DHOase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-AUG-2005, sequence version 1. 07-FEB-2006, entry version 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47492 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 VDGQKATNIFPYTAP 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VTGEKITAVLPYDAP 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=PH-1 / NRRL 31084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         445 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63
65
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Q4IFN3_GIBZE
                                                                                                                                                                                                                                                                                                                                                                                                                              Hopwood D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 METAL
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    요 . 성
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PRO0053; FORKHEAD.
PRODOM; PD000425; TF Fork head; 1.
PROSITE; SM00339; FM; 1.
PROSITE; PS00657; FORK HEAD 1; 1.
PROSITE; PS00658; FORK HEAD 2; 1.
PROSITE; PS0039; FORK HEAD 3; 1.
COMPLETE PS0039; FORK HEAD 3; 1.
TRANSCRIPTION; TRANSCRIPTION REGULATION.
SEQUENCE 279 AA; 31322 MW; 0C926B95AD122D9B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Stein L.D., Bao Z., Blasiar D., Blumenthal T., Brent M.R., Chen N., Chinwalla A., Clarke L., Clee C., Coghlan A., Coulson A., D'Eustacchio P., Fitch D.H.A., Fulton E.B., Fulton R.B., Kuwabara P.E., Marcis T.W., Hillier L.W., Kamath R., Mullikin J.C., Plumb R.W., Rogers J., Schein J.E., Minx P., Mullikin J.C., Plumb R.W., Rogers J., Schein J.E., Sohrmann M., Spieth J., Stajich J.E., Wei C., Willey D., Wilson R.K., Durbin R., Waterston R.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
GO; GO:0006350; P:transcription; IEA.
InterPro; IPR011991; Wing_hlx_DNA_bd.
PFOOXE: IPR011991; Wing_hlx_DNA_bd.
PFOOXE: IPR011991; Wing_hlx_DNA_bd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The genome sequence of Caenorhabditis briggsae: a platform for comparative genomics.";
PLOS Biol. 1:166-192(2003).
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.
-!- SUBCELLULAR LOCATION: Nuclear (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 279,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=14624247; DOI=10.1371/journal.pbio.0000045;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2000, integrated into UniProtKB/Swiss-Prot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; CAAC01000068; CAE68479.1; -; Genomic_DNA SMR; Q619H6; 101-178.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
                                                                                                                                                               23-NOV-2004, integrated into UniProtKB/TrEMBL. 23-NOV-2004, sequence version 1. 07-FEB-2006, entry version 12. Hypothetical protein CBG14280.
                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
                                                                                                                              279 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46.4%; Score 45; 57.1%; Pred. No.
                                                                                                                              PRT;
|:|| |:|
GEKARNLFVMPTFVQPYGAPG 50
                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           213 GAAAANLFPYFNPG 226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                          Caenorhabditis briggsae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
nes 8; Conserva
                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=6238;
                                                                                                                         Q619H6_CAEBR
Q619H6;
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Q9RKUS;
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Gaps

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RESULT 12
ALN STRCO
ID ALN S
AC Q9RKU
DT 01-DE

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Birren B.W., Nusbaum C., Abouelleil A., Allen N., Anderson S.,
Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavkiy L.,
Buchsgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
Choepel Y., Collymore A., Cooke P., Cooke P., Corum B., Dehrellano K.,
Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
Brickson J.F., Gardyna S., Gnerre S., Graham L., Garen-Pierre N.,
Hafez N., Hagopian D., Hagos B., Hall J., Horton L., Hulme W.,
A Raratas A., Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G.,
Lui A., Ma L.-J., Mabbitt R., Machean C., Macdonald P., Major J.,
Manning J., Mathews C., Mauceli B., McCarthy M., Meldrim J.,
Meneus L., Mihova T., Mlenga V., Murphy T., Naylor J., Nguyen C.,
Nicol R., Nielsen C.B., Norbu C., O'Connor T., O'Donnell P.,
O'Neil D., Oliver J., Peterson K., Phunkhang P., Pierre N.,
Purcell S., Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C.,
Smirnov S., Smith C., Spencer B., Schupbeack R., Seeman S., Severy P.,
Shubbe M., Talamas J., Tesfaye S., Theodore J., Topham K., Travers M.,
Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
Alander E.S.;
Lander                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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Caldicellulosiruptor saccharolyticus DSM 8903.
Bacteria; Firmicutes; Clostridia; Clostridiales; Syntrophomonadaceae; Caldicellulosiruptor.
NCBI_TaxID=351627;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T., Hammon N., Israni S., Pitluck S., Richardson P.; "Sequencing of the draft genome and assembly of Caldicellulosiruptor asccharolyticus DSM 8993.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Fusarium graminearum genome sequence.";
Submitted (FBB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 45; DB 2; Length 811; Pred. No. 2.1e+02; 0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00141; ASP PROTEASE; UNKNOWN 1.

Complete proteome; Hypothetical protein.

SEQUENCE 811 AA; 84248 MW; C2CSA4A02E10DA79 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, AACM01000168; EAA73443.1; -; Genomic_DNA.
GO; GO:0004194; F:pepsin A activity; IEA.
GO; GO:0006508; P:proteolysis; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-DEC-2005, integrated into UniProtKB/TrEMBL. 20-DEC-2005, sequence version 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=DSM 8903;
US DOE Joint Genome Institute (JGI-PGF);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro, IPR001969; Pept Asp AS.
InterPro, IPR001461; Peptidase Al.
PANTHER; PTHR13683; Peptidase Al; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           676 DDDKETATGGYTAPGKÓ 692
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Conserved membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QZZH01_CALSA PRELIMINARY;
Q2ZH01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 58.8
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00792; PEPSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        preliminary data.
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Q2ZH01_CAL
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NUCLECTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

NUCLECTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

ROSS M.T., Graffman D.V., Coffey A.J., Scherer S., McLay K., Muzny D.,

ROSS M.T., Graffman D.V., Coffey A.J., Scherer S., McLay K., Muzny D.,

Platzer M., Howell G.R., Burnows C., Bird C.P., Frankish A.,

Lovell F.L., Howe K.L., Ashurst J.L., Fulton R.S., Sudbrak R., Wen G.,

Jones M.C., Hurles M.B., Andrews T.D., Scott C.E., Searle S.,

Ramser J., Whittaker A., Deadman R., Carter N.P., Hunt S.E., Chen R.,

Ramser J., Whittaker P., Havlak P., Hodgson A., Metzker M.L.,

Rankser J., S., Scott G., Steffen D., Sodergren E., Wheeler D.A.,

Morley K.C., Ainscough R., Ambrose K.D., Ansari-Lari M.A., Aradhya S.,

Ashwell R.I., Babbage A.K., Bagguley C.L., Ballabio A., Banerjee R.,

Barker G.E., Barlow K.F., Barrett I.P., Bares K.N., Bears D.M.,

Beasley H., Beaaley O., Beck A., Bethel G., Blechschmidt K., Brady N.,

Bray-Allen S., Bridgeman A.M., Brown A.J., Brown M.J., Bonnin D.,
                                                                                                                                                                                                                                                                 Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-FEB-2006, entry version 36.
G antigen family C 1 protein (Prostate-associated gene 4 protein)
(PAGE-4) (PAGE-1) (GAGE-9).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "PAGE-1, an X chromosome-linked GAGE-like gene that is expressed normal and neoplastic prostate, testis, and uterus."; Proc. Natl. Acad. Sci. U.S.A. 95:10757-10762(1998).
                                                           STRAIN=DSM 8903;
US DDE JOIN GEOME INSTITUTE (JGI-ORNL);
Larimer F., Land M.,
"Annotation of the draft genome assembly of Caldicellulosiruptor
                                                                                                                                                                                  -!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=98393718; PubMed=9724777; DOI=10.1073/pnas.95.18.10757; Brinkmann U., Vasmatzis G., Lee B., Yerushalmi N., Essand M.,
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                                                                                                                                                                                                                                                                                                                                                                                        Length 908;
                                                                                                                                                                                                                                                                                                                                                                                          Score 45; ____Pred. No. 2.4e+02;
Submitted (OCT-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Transcription map in Xp11.23.";
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                            saccharolyticus DSM 8903.";
Submitted (NOV-2005) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                            EMBL; AALW01000031; EAP42636.1; -; Genomic_DNA.
SEQUENCE 908 AA; 105151 MW; B5E42A7161E5ED12 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-JAN-2001, integrated into UniProtKB/Swiss-Prot 01-AUG-1998, sequence version 1.
                                                                                                                                                                                                                                                                                                                                                                                        46.4%; Score 45; DB 2; 38.9%; Pred. No. 2.4e+02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  102 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=PAGE4; Synonyms=GAGEC1; ORFNames=JM27; Homo sapiens (Human).
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576 LDGYTKTNYYPYSEPTEE 593
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                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                            preliminary data.
                                          NUCLEOTIDE SEQUENCE.
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Burtond a. A., Buard F., Burton F., Burton D., Burgess J., Burton J., Bye J.W., Cared C., Charel L., Chako, J., Chang. C., Chang. C., Chang. C., Chang. C., Chang. C., Chang. C., Chang. C., Chang. C., Chang. C., Chang. C., Chang. C., Chang. C., Chang. C., Congler J., Chang. C., Chang. C., Chang. C., Congler J., Cared J. C., Congler J., Cared J. C., Chang. C., Chang. C., Chang. C., Chang. C., Daviss J., Daviss J., Daviss J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Davis J., Hurk J., Edu. J., Hurk J., Edu. J., Hurk J., Edu. J., Hurk J., Edu. J., Hurk J., Edu. J., Hurk J., Edu. J., Mordal. J., Mordal. J., Mordal. J., Mordal. J., Mordal. J., Mordal. J., Mordal. J., Mordal. J., Mordal. J., Mordal. J., Mordal. J., Mordal. J., Mordal. J., Mordal. J., Mordal. J., Mordal. J., Mordal. J., Mordal. J., Mordal. J., Mordal. J., Mordal. J., Mordal. J., Mordal. J., Mordal. J., Mordal. J., Mordal. J., Mordal. J., Mordal. J., Mordal. J., Mordal. J., Mordal. J., Mordal. J., Mordal. J., Mordal. J., Mordal. J., Mordal. J., Mordal. J., Mordal. J., Mordal. J., Mordal. J., Mordal. J., Mordal. J., Mordal. J., Mordal. J., Mordal. J., Mordal. J., Mordal. J., Mordal. J., Mordal. J., Mordal. J., Mordal. J., Mordal. J., Mordal. J., Mordal. J., Mor
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TISSUB-Placenta,

MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Rlausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Diatchenko L., Marusina K.R., Farmer A.A., Rubin G.M., Hong L.,

B Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

B Rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Robas S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Bosak S.A., McEvan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Multing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

B Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

B Carning A., Schmutz J., Myers R.M.,

B Butterfield Y.S.N., Krzywinski M.I., Schalska U., Smailus D.E.,

B Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

B Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

B Butterfield W. Schein J.E., Jones S.J.M., Marra M.A.;

B Bardenstan A., Schein J.E., Jones S.J.M., Marra M.A.;

B Bardenstan A., Schein J.E., Jones S.J.M., Marra M.A.;

B Bardenstan A., Schein J.E., Jones S.J.M., Marra M.A.;

B Branch B. M. B. M. B. M. B. M. B. M. B. M. B. M. B. M. B. M. B. M. B. M. B. M. B. M. B. M. B. M. B. M. B. M. B. M. B. M. B. M. B. M. B. M. B. M. B. M. B. M. B. M. B. M. B. M. B. M. B. M. B. M. B. M. B. M. B. M. B. M. B. M. B. M. B. M. B. M. B. M. B. M. B. M. B. M. B. M. B. M. B. M. B. M. B. M. B. M. B. M. B. M. B. M. B. M. B. M. B. M. B. M. B. M. B. M. B. M. B. M. B. M. B. M. B. M. B. M. B. M. B. M. B. M. B. M. B. M. B. M. B. M. B. M. B. M. B. M. B. M. B. M. B. M. B. M. B. M. B. M. B. M. B. M. B. M.
                           Burgess J., Burrill W.,
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Burch P., Burrel I
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TISSUE SPECIFICITY: Preferentially expressed in normal male and female reproductive tissues, prostate, testis, fallopian tube, uterus, and placenta, as well as in prostate cancer, testicular cancer, and uterine cancer.

SIMILARITY: Belongs to the GAGE family

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                                                                                                                                                                                                                                                  1 102 G antigen family C 1 protein.
/FTId=PRO 0000148348.
102 AA; 11153 MW; CE5D07AFBF73301B CRC64;
                                                                                                                                                                                                                                                                                                             45.4%; Score 44; DB 1; Length 102;
43.8%; Pred. No. 35;
Live 5; Mismatches 4; Indels
                                                         EMBL; AF275258; AAF88037.1; -; mRNA.

EMBL; AJ005894; CAA06751.1; -; mRNA.

EMBL; AF238380; -; NOT ANNOTATED CDS; Genomic_DNA.

EMBL; BC010897; AAH10897.1; -; mRNA.

Ensembl; ENSG00000101951; Homo saplens.

H-INVDB; HIX0016804; -.
                                                                                                                                                                                               InterPro; IPR008625; GAGE.
PANTHER; PTHR14047; GAGE; 1.
Pfam; PF05831; GAGE; 1.
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Les 7; Conservative
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MIM; 300287; gene.
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completed: August 30, 2006, 04:29:18 ne : 72.1818 secs Search cor Job time

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Sequence 2, Application US/09479614
; Sequence 2, Application US/09479614
; Patent No. 6573372
; GENERAL INFORMATION:
; APPLICANT: Weber, Eric
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047100 NUMBER: US/09/479,614
; CURRENT APPLICATION NUMBER: US/09/479,614
; CURRENT FILING DATE: 2000-01-07
; EARLIER PLING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 496
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US-09-479-614-14
; Sequence 14, Application US/09479614
; Sequence 14, Application US/09479614
; Patent No. 6573372
; GENERAL INFORMATION:
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; TITLE OF INVENTION: PORTION UNDER: US/09/479,614
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; SARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NOS: 34
                        Sequence 29, Appl
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Sequence 11, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 24809, Ap
Sequence 269, Appl
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US-09-612-4002-11
US-09-542-500-17
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US-10-197-220-169
US-10-055-364-46
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US-08-350-841A-1589
US-08-486-099-103
US-08-486-239-103
US-08-485-551A-103
US-08-485-551A-103
US-08-485-554A-103
US-08-473-349A-103
US-08-473-349A-103
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ORGANISM: Felis catus
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ORGANISM: Felis catus
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8106, Ap
5, Appli
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Sequence 2, Appl
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                                                                                                                                                                                   August 30, 2006, 04:31:13 ; Search time 17.8182 Seconds (without alignments) 88.424 Million cell updates/sec
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                        GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-09-701-6230-2
US-09-701-6230-2
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US-09-401-636-3
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US-09-489-039A-8106
US-10-077-699C-5
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PCT-US96-03916-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           650591 segs, 87530628 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                     OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                        US-10-758-165A-10
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Maximum DB seq length: 2000000000
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Match Length DB
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gequence 2, Application US/09701623C

Patent No. 6811782

GENERAL INFORMATION:

APPLICATION:

TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF

TITLE OF INVENTION: ALLERGY

TITLE OF INVENTION: ALLERGY

TITLE OF INVENTION: ALLERGY

TITLE OF INVENTION: ALLERGY

TITLE OF INVENTION: ALLERGY

CURRENT APPLICATION NUMBER: US/09/701,623C

CURRENT FILING DATE: 2000-12-01

PRIOR FILING DATE: 1999-06-21

PRIOR PILING DATE: 1999-06-21

PRIOR FILING DATE: 1999-06-20

NUMBER OF SEQ ID NOS: 91

SCOFTWARE: Patentin Ver. 2.1

SEQ ID NO 2

TYPE: PRI

TYPE: PRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                           NAME/KEY: misc feature
LOCATION: (451)..(451)
OTHER INFORMATION: "n" stands for any nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (500)...(500)
OTHER INFORMATION: "n" stands for any nucleic acid FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc feature
LOCATION: (853)..(853)
OTHER INFORMATION: "n" stands for any nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc feature
LOCATION: (1382)..(1382)
OTHER INFORMATION: "n" stands for any nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY: misc_feature
NOCATION: (1832) ..(1832)
OTHER INFORMATION: "n" stands for any nucleic acid
LOCATION: (136)..(136)
OTHER INFORMATION: "n" stands for any nucleic acid
                                                                                                 NAME/KEY: misc feature
LOCATION: (413)..(414)
OTHER INFORMATION: "n" stands for any nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc feature
LOCATION: (460)..(462)
OTHER INFORMATION: "n" stands for any nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: (530)...(530)
OTHER INFORMATION: "n" stands for any nucleic acid
PEATURE:
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LOCATION: (568)..(568)
OTHER INFORMATION: "n" stands for any nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc feature
LOCATION: (847)...(849)
OTHER INFORMATION: "n" stands for any nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        y Match
B9.7%; Score 87; DB 2; Lv
Local Similarity 100.0%; Pred. No. 8.8e-07;
hes 16; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 VDGQKATNIFPYTAPG 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc feature
LOCATION: (500)..(500)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-281-760E-35
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US-09-701-623C-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: (82)..(82)
UNTER INFORMATION: The 'Xaa' at location 82 stands for a stop codon, Trp, or Cys.
FEATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                    RESULT 3
US-09-479-614-29
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; Batent No. 6734287
; GENERAL INFORMATION:
; APPLICANT: Lawton, Robert
; APPLICANT: Lawton, Brion
; APPLICANT: Brancoeur, Greg
; TITLE OF INVENTION: Canine Allergy
; TITLE OF INVENTION: Canine Allergy
; TITLE OF INVENTION: Canine Allergy
; TITLE OF INVENTION: Canine Allergy
; FILE REFERENCE: 01-1275A
; CURRENT APPLICATION NUMBER: US/09/281,760E
; CURRENT PILING DATE: 1999-04-09
; RIOR FILING DATE: 1998-04-09
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 35
; LENGTH: 108
                                                                        100.0%; Score 97; DB 2; Length 496; 100.0%; Pred. No. 1.1e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   at location 81
Gln, Pro, Leu,
                                                                                                                                                0; Mismatches
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                                                                                                                                                                                                                                                         1 VDGQKATNIFPYTAPGKQ 18
                                                                                                                                                                                                                 1 VDGQKATNIFPYTAPGKQ 18
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OTHER INFORMATION: The 'Xaa'
OTHER INFORMATION: Ala, Val,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Canis familiaris
                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , ORGANISM: Felis catus US-09-479-614-29
                                                                                                            Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-281-760E-35
          US-09-479-614-2
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                                                                               Query Match
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Length 426;
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        APPLICANT: HOLLIS, GREGORY F.
APPLICANT: PATEL, MAYUR D.
TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: CHRISTINE E. CARTY
STREET: 126 E. LINCOLN AVENUE; P.O. BOX 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Synthetically generated proteins US-09-401-636-7
                                                                                                                                                                                                                                       COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13795
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89.7%; Score 87; DB 5; Le 100.0%; Pred. No. 3.9e-06;
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GENERAL INC. 0313/143

APPLICANT: Hellman, Lars T.

TITLE OF INVENTION: BEHANCED VACCINES

FILE REFERENCE: 10223/006001

CURRENT APPLICATION NUMBER: US/09/401,636

CURRENT FILING DATE: 1999-109-22

PRIOR FILING DATE: 1998-11-02

NUMBER OF SEQ ID NOS: 11

SOFTWARE: FASEESEQ FOR WINGOWS VERSION 4.0

SEQ ID NO 7

LENGTH: 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0%; Pred. No. ...
Matches 16; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: CARTY, CHRISTINE E.
REGISTRATION NUMBER: 36,099
REPERENCE/DOCKET NUMBER: 1921:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 VDGQKATNIFPYTAPGKQ 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (908) 594-6734
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             426 amino acids
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Best Local Similarity 77.8<sup>†</sup>
Matches 14<sup>‡</sup> Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                                                          COUNTRY: USA
ZIP: 07065-0907
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        single
                                                                                                                                                                                      NEW JERSEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: si
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GENERAL INFORMATION:
                                                                                                                                                             CITY: RAHWAY
STATE: NEW JE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08336583
Patent No. 5629415
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: HOLLIS, GREGORY F.
APPLICANT: PATEL, MAYUR D.
TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULIN E
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHRISTINE E. CARTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89.7%; Score 87; DB 1; Length 426; 100.0%; Pred. No. 3.9e-06; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 07065-0900
COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,583
FILING DATE: 09-NOV-1994
CLASSIFICATION: 424
                                     OTHER INFORMATION: CH2CH3n of dog IgE PUBLICATION INFORMATION: AITHORS: Patel JOURNAL: Immunogenetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY AGENT INFORMATION:
NAME: CARTY, CHRISTINE E.
REGISTRATION NUMBER: 36,099
REFERENCE/DOCKET NUMBER: 19211
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-6734
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 426 amino acids
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Best Local Similarity 100.0
....hea 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , MOLECULE TYPE: protein US-08-336-583-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                          ; VOLUME: 41
; PAGES: 282-286
; DATE: 1995
US-09-701-623C-2
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PCT-US95-13795-2
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US-08-336-583-2
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                                                                                                                                                                                                                                                                                                                                                                                           ; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 61.9%; Score 60; DB 2; Best Local Similarity 61.1%; Pred. No. 0.079; Matches 11; Conservative 3; Mismatches
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Sequence 9, Application US/09401636

Patent No. 6913749;
GENERAL INFORMATION:
TITLE OF INVENTION: ENTRANCE

FILE REFERENCE: 10223/00601

CURRENT APPLICATION NUMBER: US/09/401,636

CURRENT PLING DATE: 1999-09-22

PRIOR PILING DATE: 1999-09-22

PRIOR PILING DATE: 1999-016,552

PRIOR FILING DATE: 1998-11-02

NUMBER OF SEQ ID NOS: 11

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 9

LENGTH: 341

TYPE: NOW:
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Sequence 11, Application US/09401636

Patent No. 6913749

GENERAL INFORMATION:
TITLE OF INVENTION: ENHANCED VACCINES
FITE REFERENCE: 10223/006001

CURRENT FILING DATE: 1999-09-22

PRIOR FILING DATE: 1999-09-22

NUMBER OF SEQ ID NOS: 11

SEQ ID NO 11

LENGTH: 341

TYPE: PRT

CREATING ATTE: 1999-11-02

NUMBER: OF SEQ ID NOS: 11

SEQ ID NO 11

CREATING BATE: 1998-11-02

NUMBER: OF SEQ ID NOS: 11

SEQ ID NO 11

CREATING BATE: 1998-11-02

NUMBER: OF SEQ ID NOS: 11

CREATING BATE: 1998-11-02

NUMBER: OF SEQ ID NOS: 11

CREATING BATE: 1998-11-02

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CREATING BATE: 1998-11-02

CREATING BATE: 1998-11-0
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; RICH FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FASESEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 341
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Indels
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US-09-401-636-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 61.9%; Score 60; DB 2; Best Local Similarity 61.1%; Pred. No. 0.079; Matches 11; Conservative 3; Mismatches
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GENERAL INFORMATION:
FARE OF INVENTION:
FILE REFERENCE: 1022/006001
CURRENT APPLICATION NUMBER: US/09/401,636
CURRENT FILING DATE: 1999-09-22
FRIOR APPLICATION NUMBER: US 60/106,652
FRIOR FILING DATE: 1998-11-02
FRIOR FILING DATE: 1998-11-02
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
                                                                                                                                                                                                   Sequence 3, Application US/09401636
Fatent No. 6913749
GENERAL INPORMATION:
APPLICANT: Hellman, Lars T.
TITLE OF INVENTION: ENHANCED VACCINES
FILE REPRENCE: 10223/006001
CURRENT PILING DATE: 1999-09-22
CURRENT FILING DATE: 1999-09-22
PRIOR APPLICATION NUMBER: US 60/106,652
PRIOR APPLICATION NUMBER: US 60/106,652
PRIOR PELLING DATE: 1998-11-02
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 341
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US-09-401-636-4
; Sequence 4, Application US/09401636
; Patent No. 6913749
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61 VDGQKAENLFPYTAPPKR 78
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ORGANISM: Artificial Sequence
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US-09-401-636-3
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                                                                                       Query Match
61.9%; Score 60; DB 2; Length 341;
Best Local Similarity 61.1%; Pred. No. 0.079;
Matches 11; Conservative 3; Mismatches 4; Indels
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; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Synthetically generated proteins US-09-401-636-8
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                                                                                                                                                                                                                                                                                     RESULT 14
US-09-401-636-5
; Sequence 5, Application US/09401636
; Patent No. 6913749
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVERTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR APPLICATION NUMBER: US 60/106,652
; RANDRER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 34.2
; TYPE: PRT
; ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-401-636-8
US-09-401-636-8
Sequence 8, Application US/09401636
PARENT NO. 6913749
GENERAL INFORMATION:
APPLICANT: Hellman, Lare T.
TITLE OF INVENTION: ENHANCED VACCINES
CURRENT APPLICATION NUMBER: US/09/401,636
CURRENT APPLICATION NUMBER: US/09/401,636
CURRENT APPLICATION NUMBER: US/09/401,636
PRIOR APPLICATION NUMBER: US 60/106,652
PRIOR FILING DATE: 1999-11-02
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FRSELSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 342
                                                                                                                                                                               1 VDGQKATNIFPYTAPGKQ 18
                                                                                                                                                                                                              62 VDGQEAENLFPYTTRPKR 79
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62 VDGQEAENLFPYTTRPKR 79
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
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Search completed: August 30, 2006, 04:33:02 Job time : 17.8182 secs This Page Blank (uspto)

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TITLE OF INVENTION: IMMINOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
FILE REFERENCE: 5051-661
CURRENT APPLICATION NUMBER: US/10/758,165
CURRENT PILING DATE: 2004-01-16
PRIOR PILING DATE: 2003-01-16
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin version 3.2
SEQ ID NO 10
LENGTH: 18
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Best Local Similarity 100.
Matches 18; Conservative
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US-10-758-165-10
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1. /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2. /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
3. /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
4. /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US108_PUBCOMB.pep:*
5. /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US108_PUBCOMB.pep:*
6. /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US108_PUBCOMB.pep:*
                                                                                                                            August 30, 2006, 04:33:28; Search time 90.9091 Seconds (without alignments) 91.717 Million cell updates/sec
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GenCore version 5.1.9
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Maximum Match 100%
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Score 97; DB 5; I Pred. No. 6.2e-09; ; Mismatches 0;

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29	9	61.9	341	4	US-10-176-664-11	Ξ,
30	9	61.9	341	4	US-10-673-594-3	m
31	9	61.9	341	4	US-10-673-594-4	4
32	9	61.9	341	4	US-10-673-594-6	9
33	9	61.9	341	4	US-10-673-594-9	6
34	9	61.9	341	4	US-10-673-594-11	1,
35	9	61.9	342	m	US-09-401-636-5	Ŋ
36	9	61.9	342	٣		æ
37	09	61.9	342	4	US-10-176-664-5	Ŋ
38	9	61.9	342	4	US-10-176-664-8	8
39	9	61.9	342	4	US-10-673-594-5	'n
40	9	61.9	342	4	US-10-673-594-8	Sequence 8, Appli
41	9	61.9	345	m	US-09-401-636-10	70
42	9	61.9	345	4	US-10-176-664-10	70
43	9	61.9	345	4	US-10-673-594-10	2
44	9	61.9	347	4	US-10-438-794-14	14
45	9	61.9	347	4	US-10-453-915-14	14,
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; Sequence	10, 1	Applic	Sequence 10, Application US/10758165	710	758165	
, Publicat	ion No	o usa	Publication No. US20050196816A1	16A	. 4	
GENERAL INFORMATION:	INFOR	ATION		;		

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RESULT 6
US-10-214-524-25
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Sequence 14, Application US/20030216565A1

GENERAL INFORMATION:
   APPLICANT: McCall, Catherine
   APPLICANT: Weber, Eric
   TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
   FILE REFERENCE: P-1047
   CURRENT PAPLICATION NUMBER: US/10/409,772
   CURRENT PAPLICATION NUMBER: US/09/479,614
   PRIOR APPLICATION NUMBER: US/09/479,614
   NUMBER OF SEQ ID NOS: 34
   SOFTWARE: PatentIn Ver. 2.0
   SEQ ID NO 14
   LENGTH: 431
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APPLICANT: McCall, Catherine
APPLICANT: Weber, Eric
TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
FILE REFERENCE: P-1047
CURRENT PAPLICATION NUMBER: US/09/479,614
CURRENT FILING DATE: 1999-01-07
EARLIER APPLICATION NUMBER: 60/115,033
EARLIER FILING DATE: 1999-01-07
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
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     100.0%; Score 97; DB 3; Length 431; 100.0%; Pred. No. 2e-07; ive 0; Mismatches 0; Indels
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100.0%; Pred. No. 2.4e-07;
tive 0; Mismatches 0;
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; Sequence 29, Application US/09479614
; Publication No. US20030013183A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 2, Application US/09479614; Publication No. US20030013183A1
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Best Local Similarity 100.0
Warches 18; Conservative
Query Match
Best Local Similarity 100.'
Matches 18; Conservative
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ORGANISM: Felis catus
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Matches 18; Conserv
                                                                                                                                                                              RESULT 3
US-10-409-772-14
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Sequence 25, Application US/10214524

Sequence 25, Application US/10214524

Publication No. US20030073142A1

GENERAL INFORMATION:

APPLICANT: Vang, Yong-Amin

APPLICANT: Chen, Swey-Shen Alex

APPLICANT: Chen, Swey-Shen Alex

APPLICANT: Chen, Sung-Min

APPLICANT: Chen, Zhong

ITILE OF INVENTION: IMMUNGGLOBULIN E VACCINES AND METHODS OF USE THEREOF

FILE REPERBNCE: IGE-0010.1.P.1.1

CURRENT APPLICATION NUMBER: US/10/214,524

CURRENT FILING DATE: 2000-08-08

PRIOR PILING DATE: 2001-08-13

NUMBER: OF SEQ ID NOS: 61

SEQ ID NO 25

LENGTH: 496
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APPLICANT: McCall, Catherine
APPLICANT: Weber, Eric
TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
FILE REPERENCE: P-1047
CURRENT APPLICATION NUMBER: US/09/479,614
CURRENT APPLICATION NUMBER: 60/115,033
EARLIER APPLICATION NUMBER: 60/115,033
SEALIER PLING DATE: 1999-01-07
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 29
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APPLICAMY: Weber, Eric
TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
FILE REFRENCE: P-1047
CURRENT APPLICATION NUMBER: US/10/409,772
CURRENT PILING DATE: 2003-04-07
PRIOR FILING DATE: 2000-01-07
RINGRED OF SEQ ID NOS: 34
SUMBER OF SEQ ID NOS: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 2, Application US/10409772; Publication No. US20030216565A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  216 VDGQKATNIFPYTAPGKQ 233
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US-10-214-524-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100.0
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Felis catus
US-09-479-614-29
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AUTHORS: Patel,
JOURNAL: Immunogenetics
VOLUME: 41
PAGES: 282-286
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US-10-723-207-2
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**Bublication No. US20030216565A1

**Publication No. US20030216565A1

**Sequence 29, Application US/10409772

**Sequence 20, Application US/1040972

**APPLICANT: Weber, Eric

**TITE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods

**TITE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods

**TITE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods

**TITE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods

**TITE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods

**TITE OF INVENTION: STORED: 2003-04-07

**NUMBER OF SEQ. ID NOS: 34

**SOFTWARE: Patentin Ver. 2.0

**TEMPLICANT: APPLICANT: PAPILICANT: PAPIL
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; Publication No. US20050196816A1
; GENERAL INFORMATION:
    GENERAL INFORMATION:
    APPLICANT: Hammerberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT APPLICATION NUMBER: US/10/758,165
; CURRENT PILING DATE: 2004-01-16
; PRIOR PILING DATE: 2003-01-16
; RIOR FILING DATE: 2003-01-16
; SRO ID NO 9: 16
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 9
; LENGTH: 18
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Pred. No. 2.9e-07;
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100.0%; Pred. No. 2.4e-07;
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100.0%; Pre
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Best Local Similarity 100.0
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; ORGANISM: Pelis catus
US-10-409-772-29
                                                         ; TYPE: PRT
; ORGANISM: Felis catus
US-10-409-772-2
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Best Local Similarity
Matches 16; Conserva
SEQ ID NO 2
LENGTH: 496
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Sequence 2, Application US/10723207

| Sequence 2, Application US/10723207
| Publication No. US20050250934A1
| GENERAL INFORMATION:
| APPLICANT: Walfield, Alan M. | ITLE OF INVENTION: BEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF TITLE OF INVENTION: ALLERGY
| FILE REFERENCE: 1151-4153US2 | UNRERT PRILICE OF INVENTION: ALLERGY FILING DATE: 2003-11-24 |
| PRIOR APPLICATION NUMBER: 09/701,623 |
| PRIOR PILING DATE: 1999-06-21 |
| PRIOR PILING DATE: 1999-6-21 |
| PRIOR PILING DATE: 1999-6-21 |
| PRIOR PILING DATE: 1999-6-21 |
| PRIOR PILING DATE: 1999-6-21 |
| PRIOR PILING DATE: 1999-6-21 |
| PRIOR PILING DATE: 1999-6-21 |
| PRIOR PILING DATE: 1998-6-20 |
| WUMBER OF SEQ ID NOS: 91 |
| SOFTWARE: PATENTIN VOS: 91 |
| SEQ ID NO 2 |
| FEATURE: OTHER INFORMATION: CH2CH3n of dog 19E |
| PUBLICATION INFORMATION: PATENTIAN INFORMATION: PATENTIAN INFORMATION: PATENTIAN INFORMATION:
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1 Sequence 28, Application US/10214524

2 Sequence 28, Application US/10214524

3 Fublication No. US20030073142A1

3 Fublication No. US20030073142A1

3 APPLICANT: Chen, Swey-Shen Alex

4 APPLICANT: Chen, Sheny Min

5 APPLICANT: Chen, Zhong

7 TITLE OF INVENTION: IMMUNOSLOBULIN E VACCINES AND METHODS OF USE THEREOF

7 FILE REFERENCE: IGE-00101.P.1.1

7 CURRENT APPLICATION NUMBER: US/10/214,524

7 CURRENT PILING DATE: 2002-08-08

7 FILE REFERENCE: 2001-08-13

7 NUMBER OF SEQ ID NOS: 61

7 SEQ ID NO 28

7 LENGTH: 426
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89.7%; Score 87; DB 4; Le
Best Local Similarity 100.0%; Pred. No. 9.3e-06;
Matches 16; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89.7%; Score 87; DB 5; Le
100.0%; Pred. No. 6.6e-06;
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; ORGANISM: Dog (Canis familiaris)
US-10-214-524-28
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Les 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Synthetically generated proteins
US-10-176-664-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Synthetically generated proteins US-09-401-636-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 79.4%; Score 77; DB 3; I Best Local Similarity 77.8%; Pred. No. 0.00034; Matches 14; Conservative 2; Mismatches 2;
                                                                                 Sequence 7, Application US/09401636
Sequence 7, Application US/09401636
Fatent No. US20010038843A1
GENERAL INFORMATION:
APPLICANT: Hellman, Lars T.
TITLE OF INVENTION: ENHANCED VACCINES
FILE REFERENCE: 10223/006001
CURRENT APPLICATION NUMBER: US/09/401,636
CURRENT FILING DATE: 1999-09-22
FRIOR FILING DATE: 1998-11-02
NUMBER OF SEQ ID NOS: 11
SOUTHWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
LENGTH: 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7, Application US/10176664

Publication No. US20030031663A1

GENERAL INFORMATION:
APPLICANT' Hellman, Lars T.
TITLE OF INVENTION: ENHANCED VACCINES
FILE REFERENCE: 10223/006001

CURRENT APPLICATION NUMBER: US/10/176,664

CURRENT FILING DATE: 2002-06-19

PRIOR APPLICATION NUMBER: US/09/401,636

PRIOR APPLICATION NUMBER: US/09/401,636

PRIOR APPLICATION NUMBER: US/09/401,636

PRIOR APPLICATION NUMBER: US/09/401,636

PRIOR PILING DATE: 1999-01-02

NUMBER OF SEQ ID NOS: 11

SOFTWARE: FASLSEQ for Windows Version 4.0

SEQ ID NO 7

LENGTH: 343
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GENERAL INFORMATION: APPLICANT Hellman, Lare T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 VDGQKATNIFPYTAPGKQ 18
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61 VDGQKAENLFPYTAPPKR 78
146 VDGQKATNIFPYTAPG 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity
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US-10-673-594-7
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US-10-214-524-29

Sequence 29, Application US/10214524

Sequence 29, Application US/10214524

Fublication No. US20030073142A1

GENERAL INFORMATION:
APPLICANT: Chen, Swey-Shen Alex
APPLICANT: Chen, Swey-Shen Alex
APPLICANT: Chen, Zhong
TITLE OF INVENTION: IMMUNOSLOBULIN E VACCINES AND METHODS OF USE THEREOF
TITLE OF INVENTION: IMMUNOSLOBULIN E VACCINES AND METHODS OF USE THEREOF
TITLE OF INVENTION: UNMBER: US/10/214,524

CURRENT FILING DATE: 2001-08-08

PRIOR PLING DATE: 2001-08-13

NUMBER OF SEQ ID NOS: 61

SOFTWARE: Patentin version 3.1

SEQ ID NO 29

LENGTH: 577
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79.4%; Score 77; DB 4; Length 577;
Best Local Similarity 77.8%; Pred. No. 0.0006;
Matches 14; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 79.4%; Score 77; DB 4; Length 343 Best Local Similarity 77.8%; Pred. No. 0.00034; Matches 14; Conservative 2; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                     ; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-10-673-594-7
TITLE OF INVENTION: ENHANCED VACCINES
FILE REFERENCE: 10223/006001
CURRENT APPLICATION NUMBER: US/10/673,594
CURRENT FILING DATE: 2003-09-29
PRIOR APPLICATION NUMBER: US/09/401,636
PRIOR FILING DATE: 1999-09-22
PRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
LENGTH: 343
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                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
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2450, Ap 1112, Ap 19986, A 2022, Ap 3689, Ap 728, App 17560, A 1378, App

14, Appl 12046, A 2402, Ap 6386, Ap 11265, A

1293, Ap 50315, A 44839, A

us-10-758-165a-10.rapbn

Perfect score:

<u>e</u>

Sequence:

Scoring table:

Minimum DB 8 Maximum DB 8

Database

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Sequence 726, Application US/10471571A

Publication No. US20060115490A1

GENERAL INFORMATION:

APPLICANT: CHIRON SpA

TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS

TITLE OF INVENTION NUMBER: US/10/471,571A

CURRENT APPLICATION NUMBER: US/10/471,571A

CURRENT APPLICATION NUMBER: G803-09-12

PRIOR FILING DATE: 2001-03-27

NUMBER OF SEQ ID NOS: 5642

SOFTWARE: SeqWin99, version 1.03

SEQ ID NO 726

LENGTH: 254
                                                                                                                          Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Seq
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US-11-330-403-6482
j Sequence 6482, Application US/11330403
j Publication No. US20060159563A1
j GENERAL INFORMATION:
j APPLICANT: Abad, Mark S.
j TITLE OF INVENTION: Genes and Uses for Plant Improvement
j FILE REFERENCE: 38-21(53629)B
j CURRENT APPLICATION NUMBER: US/11/330,403
j CURRENT PILING DATE: 2006-01-12
j NUMBER OF SEQ ID NOS: 19250
j SEQ ID NO 6482
libroth: 644
j TYPE: PRT
j CRGANISM: Xanthomonas axonopodis pv. glycines
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Pred. No. 8.8;
0; Mismatches 1; Indels
                         US-10-471-571A-1112
US-11-056-35-B-19986
US-11-330-403-36-89
US-11-330-403-36-89
US-11-330-403-15-600
US-11-330-403-15-600
US-11-330-403-1378
US-11-35-233-14
US-11-330-403-1386
US-11-330-403-6386
US-11-330-403-18255
US-11-330-403-18255
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US-11-056-355B-44839
US-11-056-355B-46211
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NAME/KEY: MISC_FEATURE
LOCATION: (1)..(254)
OTHER INFORMATION: serine protease
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TYPE: PRT
ORGANISM: Staphylococcus aureus
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Best Local Similarity 88.9%;
Matches 8; Conservative (
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|KDTNIFPYT 66
US-10-471-571A-726
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Sequence 1503, Ap
Sequence 15035, A
Sequence 6, Appli
Sequence 15230, A
Sequence 15230, A
Sequence 15230, A
Sequence 15597, A
Sequence 59400, A
Sequence 5963, Ap
Sequence 5963, Ap
Sequence 5963, Ap
Sequence 5963, Ap
Sequence 5963, Ap
Sequence 5963, Ap
Sequence 19538, A
Sequence 19538, A
Sequence 19539, A
Sequence 19538, A
Sequence 19539, A
Sequence 19539, A
Sequence 19539, A
Sequence 19539, A
Sequence 19539, A
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1: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pep:*

2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
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US-11-330-403-15095
US-11-349-013-15095
US-11-342-171-6
US-11-330-403-14312
US-11-330-403-1539
US-11-330-403-1539
US-11-330-403-15597
US-11-953-349-19539
US-11-953-349-5961
US-10-953-349-5961
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                    OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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97
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                              43.3%; Score 42; DB 7; Length 644; 52.9%; Pred. No. 37; 1ive 3; Mismatches 3; Indels
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43.3%; Score 42; DB 7; Length 644;
Best Local Similarity 52.9%; Pred. No. 37;
Matches 9; Conservative 3; Mismatches 3; Indels
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43.3%; Score 42; DB 6; Length 697;
Best Local Similarity 47.1%; Pred. No. 40;
Matches 8; Conservative 1; Mismatches 8; Indels
                                                                                                                                                                                                              Sequence 15095, Application US/11330403
; Publication No. US20060159563A1
; GENERAL INFORMATION:
    APPLICANT: Abad, Mark S.
    TITLE OF INVENTION: Genes and Uses for Plant Improvement
    FILE REPERENCE: 38-21(53629)B
; CURRENT APPLICATION NUMBER: US/11/330,403
; CURRENT FILING DATE: 2006-01-12
; NUMBER OF SEQ ID NOS: 19250
; SEQ ID NO 15095
; LENGTH: 644
                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Xanthomonas axonopodis pv. citri str. 306
US-11-330-403-15095
                                                                                                                       | :|| :||| :|||||
212 DRYEATLGQVFPHTAPG 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    212 DRYEATLGOVFPHTAPG 228
                                                                                                 2 DGQKAT--NIFPYTAPG 16
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                                                                 Conservative
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; ORGANISM: Oryza sativa
US-10-449-902-38427
                                              Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                     US-11-330-403-15095
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US-11-330-403-6482
                                 Query Match
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RESULT 5 US-11-342-171-6

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US-11-342-171-66

Sequence 66, Application US/11342171

Publication No. US20060111558A1

PUBLICANT: Wild, Martha A.

APPLICANT: Wild, Mark D.

ITTLE OF INVENTION: RECOMBINANT INFECTIOUSLARYNGOTRACHEITIS VIRUS

TITLE OF INVENTION: AND USES THEREOF

CORRESPONDENCES: 72

CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: Cooper & Dunham LLP

STREET: 1185 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
Sequence 6, Application US/11342171
Publication No. US20060111558A1
GENERAL INFORMATION:
APPLICANT: Wild, Martha A.
APPLICANT: Cochran, Mark D.
TITLE OF INVENTION: RECOMBINANT INFECTIOUSLARYNGOTRACHEITIS VIRUS
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/342,171
FILING DATE: 27-DAN-2006
CLASSIPTCATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/468,190
FILING DATE: 06-JUN-1995
CLASSIPTCATION DATA:
APPLICATION NUMBER: US 08/126,597
FILING DATE: 24-SEP-1993
ATTORNEY/AGNT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 39.678
REGISTRATION NUMBER: 39.16-A
TELECOMMUNICATION NUMBER: 39.16-A
TELECOMMUNICATION NUMBER: 39.16-A
TELECOMMUNICATION NUMBER: 39.16-A
                                                                                                                                                                                                                            E: Cooper & Dunham LLP
1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      416 GESENTLFPTTAPG 429
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COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
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STATE: New York
COUNTRY: U.S.A.
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CURRENT APPLICATION NUMBER: US/11/330,403
CURRENT FILING DATE: 2006-01-12
NUMBER OF SEQ ID NOS: 19250
LENGTH: 582
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Best Local Similarity 57.9%;
Matches 11; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Pisum sativum
US-11-330-403-15597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CRGANISM: Glycine max US-10-953-349-19539
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-11-330-403-14312
; Sequence 14312, Application US/11330403
; Publication No. US20060159563A1
; GENERAL INFORMATION:
    TILLE OF INVENTION: Genes and Uses for Plant Improvement
; TILLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 39-21 (53629) B
; CURRENT APPLICATION NUMBER: US/11/330,403
; CURRENT FILING DATE: 2006-01-12
; NUMBER OF SEQ ID NOS: 19250
; SEQ ID NO 14312
; LENGTH: 582
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Publication No. US20060159563A1
GENERAL INFORMATION:
APPLICANT: Abad, Mark S.
TITLE OF INVENTION: Genes and Uses for Plant Improvement;
FILE REFERENCE: 38-21(53629)B
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                            Score 42;
Pred. No. 9
                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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416 GESENTLFPTTAPG 429
    Floppy disk
                                                                                                                                                                                                                                                                                                                                                       : 985 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Populus tomentosa
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Best Local Similarity 50.0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   , MOLECULE TYPE: protein US-11-342-171-66
                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
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US-11-330-403-15230
    MEDIUM TYPE:
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Sequence 19539, Application US/10953349

Publication No. US20060107345A1

GENERAL INFORMATION:
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRACMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REPRENCE: 2750-15799US2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40552
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                                                                                                                                                                                 Length 582;
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Publication No. US20060159563A1
GENERAL INFORMATION:
APPLICANT: Abad, Mark S.
TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REPREBRUCE: 38-21(55629)B
CURRENT APPLICATION NUMBER: US/11/330,403
CURRENT FILING DATE: 2006-01-12
NUMBER OF SEQ ID NOS: 19250
SEQ ID NO 15597
LENGTH: 582
                                                                                                                                                                                 DB 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 40.2%; Score 39; DB 6; Best Local Similarity 44.4%; Pred. No. 65; Matches 8; Conservative 2; Mismatches 8
TYPE: PRT
ORGANISM: Populus tremula x Populus tremuloides
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(582)
OTATION: (1)..(582)
COTATION: (1)..(582)
US-11-330-403-15230
                                                                                                                                                                            Query Match
42.8%; Score 41.5; L
Best Local Similarity 57.9%; Pred. No. 40;
Matches 11; Conservative 0; Mismatches
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Pred. No. 60;
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                                                                                                                                                                                                                                                                            1 VDGOKATNIFPYTA---PG 16
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Sequence 5961, Application US/10953349

Publication No. US20060107345A1

GENERAL INFORMATION:

APPLICANT: ALEXANDROV, Nickolai et al.

TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

TITLE OF INVENTION: ENCONDED THERBY

TITLE OF INVENTION: ENCONDED THERBY

TITLE OF INVENTION: USA01879

CURRENT PELLORICATION UNMBER: USA10/953,349

CURRENT FILING DATE: 2004-09-30

NUMBER OF SEQ ID NOS: 40252

SOFTWARE: Patentin version 3.3

SEQ ID NO 5961

LENGTH: 374
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TITLE OF INVENTION: SEQUENCE-DETERAINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
TITLE OF INVENTION: ENCONDED THERBY
TITLE OF INVENTION: ENCONDED THERBY
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PATENTIN VETSION 3.3
SEQ ID NO 19338
LENGTH: 404
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ced. No. 73;
Mismatches 8
                                                                                                                                                                                                                                                DB 6;
67;
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67;
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Pred. No.
PILE REFERENCE: 2750-1579PUS2
CURRENT PEPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 5962
LENGTH: 372
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; ORGANISM: Arabidopsis thaliana
US-10-953-349-5961
                                                                                                                                                ; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-5962
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ilarity 54.5%;
Conservative
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Best Local Similarity 44.4%;
Matches 8; Conservative
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Best Local Similarity 54.5%;
Matches 6; Conservative
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352 GEKIVNLIPYT 362
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Best Local Similarity
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Publication No. US20060107345A1
GRNERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUSS
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 5963
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; Publication No. US20060107345A1
; GENERAL INFORMATION:
; TIPLEONT: ALEXANDROY, Nickolai et al.
; TIPLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
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                                                                                                                                                                           APPLICANT: Brover, Vyacheslav
APPLICANT: Brover, Vyacheslav
APPLICANT: Alexandrov, Nickolai
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENCE: 2750-1590FUS2
CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2005-02-14
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR PILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
SEQ ID NO 55400
LENGTH: 361
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Pred. No. 65;
2; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: peptide

LOCATION: (1)..(361)

JOHTER INPORMATION: Ceres Seq. ID no. 14307779

US-11-056-355B-59400
                                                                                                           ; Sequence 59400, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
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      124 VDGKKVKRKHPYTEKEKE 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT; ORGANISM: Arabidopsis thaliana
US-10-953-349-5963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vucir Match
Best Local Similarity 44.4%;
Matches 8; Conservative 2
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Best Local Similarity 54.5
Matches 6; Conservative
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ORGANISM: Glycine max
                                                                                             JS-11-056-355B-59400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
US-10-953-349-5962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-953-349-5963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
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      셤
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

Run on:

August 30, 2006, 04:29:42; Search time 10.7273 Seconds (without alignments) 161.448 Million cell updates/sec

1 IDGQKVDEQFPQHGLVKQ 18 US-10-758-165A-11 96 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	,				
	gier.				
Score	Match	Length	BB	OI	Description
49	51.0) 616	7	E85508	hypothetical prote
49	51.	0 616	7	E90657	hypothetical prote
47			~	JC7557	lipidosin - mouse
46			N	AG3034	inositol monophosp
46	٠		N	E98251	similar to mlcb177
45	•		н	RGBYS3	regulatory protein
43	٠		~	T42322	hypothetical prote
43	44.8		~	G83358	probable ATP-bindi
43	٠		7	H86717	hypothetical prote
42	•		~	D95115	thioredoxin family
42	•		7	H97984	conserved hypothet
42	•		~	S76407	phosphoribosylanth
42	•		N	T21777	hypothetical prote
42	٠		~	T06532	pyruvate dehydroge
42	•		~	835157	
42	•		~	E69498	hypothetical prote
42	•		7	T16409	hypothetical prote
42	43.8		~	A54970	tensin, cardiac mu
41	42.		~	H72459	probable ribosomal
41	42.		Н	S76736	hypothetical prote
41	42.	305	~	F86744	tagatose-6-phospha
41	42	7 419	~	G84503	hypothetical prote
41	42.		~	T37791	probable rna polym
41	42.	_	7	T07969	probable reticulin
41	42.	_	~	T31798	hypothetical prote
41	42.	~	~	AE0701	tetrathionate redu
41	42.	_		A96669	
41	٠			E70522	probable polyketid
0.5	42.	2 237	7	AB0372	phosphoribosylamin
	'	. 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	44444444444444444444444444444444444444	44444444444444444444444444444444444444	44.6 44.9 15.9 4.4 4.6 4.7 4.9 6.7 5.9 6.4 4.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9 6.7 5.9

hypothetical prote	thioredoxin-like p	cytochrome-c oxida	hypothetical prote	ribosome releasing	hypothetical prote	hypothetical prote	transcription regu	sugar ABC transpor	hypothetical prote	cobyric acid synth	phage related prot	interferon alpha r	vrlK protein - Dic	projectin - fruit	phosphomannomutase
E71264	T46168	T43834	G89799	A64248	E83447	T21714	F83426	A96234	AC3052	AB2103	B97040	S27387	T17390	T13931	AC1384
7	~	~	7	N	~	~	7	~	7	7	7	~	7	7	~
30	132	156	181	183	183	229	324	489	489	493	531	260	1243	6658	576
	_	7	7	7	7	7	7	7	7	7	7	7	7	7	~
41.7	41.7	41.	41.	41.	41.	41.	41.	41.	41.	41.	41.	41.	41.	41.	41
40 41.7	40 41.7	40 41.		_	_	40 41.	_	_	40 41.	40 41.	40 41.	40 41.	40 41.	40 41.	39.5 41

ALIGNMENTS

	RESULT 1
	E85508
	hypothetical protein Z0260 [imported] - Escherichia coli (strain O157:H7, substrain EDL9
	C;Species: Escherichia coli
	C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
	C; Accession: E85508
	R; Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
	iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
	Nature 409, 529-533, 2001
	A; Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
	A; Reference number: A85480; MUID:21074935; PMID:11206551
	A; Accession: E85508
	A;Status: preliminary
	A; Molecule type: DNA
•	A;Residues: 1-616 <sto></sto>
	A; Cross-references: UNIPROT: Q8X7U6; UNIPARC: UPI00000D09F5; GB: AE005174; NID: 912512966; P
	A; Experimental source: strain 0157:H7, substrain EDL933
	C.Genetics.

C;Genetics:

A;Gene: Z0260 C;Superfamily: uncharacterized conserved protein

.. Length 616; Indels .. 0 51.0%; Score 49; DB 2; llarity 50.0%; Pred. No. 3.4; Conservative 6; Mismatches C Query Match Best Local Similarity Matches 8; Conserv

ij

Gaps

||::::||: |||:| QKIEDEFPELTHGLIK 73 4 OKVDEQFPQ--HGLVK 17 28 g 8

RESULT 2

hypothetical protein ECs0229 [imported] - Escherichia coli (strain O157:H7, substrain RI. C;Species: Escherichia coli C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004

C;Accession: E90657

HayAshi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001

A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomaly A;Reference number: A99629; MUID:21156231; PMID:11258796

A;Accession: E90657

A,Status: preliminary A,Molecule type: DNA A,Residues: 1-616 «HAX> A,Cross-references: UNIPROT:08X7U6; UNIPARC:UPI00000D09F5; GB:BA000007; PIDN:BAB33652.1; A,Experimental source: strain 0157:H7, substrain RIMD 0509952

A;Gene: ECs0229 C;Superfamily: uncharacterized conserved protein

51.0%; Score 49; Query Match

Length 616; DB 2;

g

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similar to mlcb1779.29 (probable monophosphatase gene) in mycobacterium leprae [imported.
C;Species: Agrobacterium tumefaciens
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
                                                                                                          C;Accession: E99251
R;Godner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum: A;Reference number: A97359; WUID:21608551; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPROT:P22579; UNIPARC:UPI0000052F61; EMBL:274746; NID:g1419766; PI)
A;Experimental source: strain $288C
A;Experimental source: strain $288C
A;Experimental source: strain $288C
A;Mang, H.; Clark, I.; Nicholson, P.R.; Herskowitz, I.; Stillman, D.J.
Mol. Cell. Biol. 10, 5927-5936, 1990
A;Title: The Saccharomyces cerevisiae SIN3 gene, a negative regulator of HO, contains for A;Reference number: A36381; MUID:91042523; PMID:2233725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-510, AQ', 511-1536 <WAN>
A; Cross-references: UNIPARC:UP10000168D4F; GB:M36822; NID:g172093; PIDN:AAA34839.1; PID::
R; Vidal, M.; Srrich, R.; Esposito, R.E.; Gaber, R.F.
A; Vidal, M.; Strich, R.; Esposito, R.E.; Gaber, R.F.
A; Title: Biol. 11, 6306-6316, 1991
A; Title: RPD! (SIN3/MME4) is required for maximal activation and repression of diverse y, A; Reference number: A41957; MUID:92049361; PMID:1944290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 227-285;414-441,'DE',444-472;667-725;1140-1200 «VID»
A;Cross-references: UNIPARC:UPI0000174911; UNIPARC:UPI0000174912; UNIPARC:UPI0000174913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:Q8U945; UNIPARC:UPI0000D237F; GB:AE007870; PIDN:AAK89535.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     regulatory protein SIN3 - yeast (Saccharomyces cerevisiae)
NiAlternate names: protein 02385; protein YOL004w
C;Species: Saccharomyces cerevisiae
C;Date: 30-Sep-1991 #sequence revision 02-Aug-1996 #text_change 09-Jul-2004
C;Accession: S66684
A;Hughes, B.; Pohl, T.M.
submitted to the Protein Sequence Database, July 1996
A;Reference number: S66685
A;Accession: S66686
A;Accession: S66686
A;Accession: S66896
A;Residues: 1-1536 cHUG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 297;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: SGD:SIN3; SD11; UME4; RPD1; MIPS:YOL004w
A;Cross-references: SGD:S0005364; MIPS:YOL004w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
46.9%; Score 45; DB
Best Local Similarity 53.3%; Pred. No. 46;
Matches 8; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Map position: 15L
C;Superfamily: regulatory protein SIN3
(Keywords: nucleus; transcription regulation
F;480-519/Region: glutamine-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47.9%; Score 46; 54.5%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Superfamily: suppressor protein suhB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Gene: AGR L 1926
A,Map position: linear chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 54.5
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ::|:|||||::
94 IEERFPQHGIL 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 VDEQFPQHGLV 16
                                                                                                                                                                                                                                                                                                                                                    A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-297 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: A36381
                                                                                                                                                                                                                                                                                                                            A;Accession: E98251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C, Genetics
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C; Species: Agrobacterium tumefaciens
C; Species: Agrobacterium tumefaciens
C; Species: Agrobacterium tumefaciens
C; Stacession: Agroba;
R; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
R; Wood, D.W.; Setubal, Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
Science 294, 2317-2323, 2001.
A; Atthors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Accession: JC7557
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Cooss.references: UNIPROT:Q99PUS; UNIPARC:UPI000017A518
C;Comment: This protein possesses long-chain acyl-CoA synthetase activity and catalyzes
C;Comment: This protein possesses long-chain acyl-CoA synthetase activity and catalyzes
circin and the impairment of fatty acid metabolism in X-linked adrenoleukodystrophy. This
C;Keywords: adrenoleukodystrophy
                                                                                                                                                                                                                                                                                         jūrīsīī

lipidosin - mouse
NyAlternate names: lipidosis-related protein
NyAlternate names: lipidosis-related protein
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
C;Accession: JGr557, Hida, A.; Inagawa-Ogashiwa, M.; Wada, M.R.; Sugiyama, K.; Shimizu, J.R;Morlya-Sato, A.; Hida, A.; Inagawa-Ogashiwa, M.; Wada, M.R.; Sugiyama, K.; Shimizu, J.R;Morlya-Sato, A.; Hida, A.; Inagawa-Ogashiwa, M.; Mada, M.R.; Sugiyama, K.; Shimizu, J.R;Title: Novel acyl-CoA synthetase in adrenoleukodystrophy target tissues.
A;Reference number: JCT557; MUID: 20563802; PMID:11112418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Experimental source: strain C58 (Dupont)
A; Experimental source: strain C58 (Dupont)
A; Gene: Atu3885
A; Map position: linear chromosome
C; Superfamily: suppressor protein suhB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ster, E.W.
Ayfitle: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens CS8.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AG3034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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Pred. No. 4.2;
5; Mismatches
   50.0%; Pred. No. 3.4; ive 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 49.0%; Score 47; DB Best Local Similarity 53.3%; Pred. No. 8.9; Matches 8; Conservative 3; Mismatches
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58 QKIEDEFPELTHGLIK 73
                                                                                                4 OKVDEQFPQ--HGLVK 17
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Best Local Similarity 54.5
                                         8; Conservative
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59 IEERFPQHGIL 69
Best Local Similarity
Matches 8; Conserv
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C,Accession: H99984

R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; E
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; E
R;Lebalanc, D.J.; Leef, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M.
y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234
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A;Gene: spr0904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C;Accession: D95115
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Reference number: A95000; MUID:21357209; PMID:11463916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Cross-references: UNIPROT.Q97R36; UNIPARC:UPI0000051693; GB:AE005672; PIDN:AAK75117.1; A,Experimental source: strain TIGR4
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                                      UNIPARC: UPI00000C68D4; GB: AE005176; PID: g12723660;
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C.Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                             Length 654;
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Pred. No. 14;
                                                                                                                                                                                                                                        44.8%; Score 43; DB 43.8%; Pred. No. 39; iive 4; Mismatches
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                                  A;Cross-references: UNIPROT:09CH17; LA;Experimental source: strain IL1403 C;Genetics:
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                                                                                                                                                                                                                                                                               Best Local Similarity 43.8
Matches 7; Conservative
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Best Local Similarity 66.7
Matches 8; Conservative
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Best Local Similarity
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A, Residues: 1-191 < KUR>
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A;Molecule type: DNA
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A; Status: preliminary
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                                                                                                                                                                                                                                             Query Match
                                                                                                                                                           A; Gene: yhfB
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C;Accession: G83358
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathchaptacesion: G83358
A;Accession: G83358
A;Accession: G83358
A;Accession: DNA
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Hypotherical protein yhfB [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
hypotherical protein yhfB [imported] - Lactococcus lactis subsp. lactis
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C;Accession: H86717
R;Bolotin, A; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrli
A;Title: The Complete genome sequence of the lactic acid bacterium Lactococcus lactis ss
A;Reference number: A86625; MUID:21235186; PMID:11337471
                                                                                                                                                                                                                                                                       hypothetical protein - phage SPP1
C;Species: phage SPP1
C;Species: phage SPP1
C;Species: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T42322
R;Alonso, J.C.; Luder, G.; Stiege, A.C.; Chai, S.; Weise, F.; Trautner, T.A.
R;Alonso, J.C.; Luder G.; Stiege, A.C.; Chai, S.; Weise, F.; Trautner, T.A.
A;Title: The complete nucleotide sequence and functional organization of Bacillus subtil
A;Reference number: Z22137; MUID:98094274; PMID:9434185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:Q91111; UNIPARC:UPI0000C5650; GB:AE004655; GB:AE004091; NIC C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: UNIPROT: 048482; UNIPARC: UP1000009B161; EMBL: X97918; PIDN: CAA66529.1
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A;Molecule type: DNA
A;Residues: 1-105 <ALO>
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Pred. No. 15;
4; Mismatches
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                                           44.48;
1 IDGQKVDEQFPQHGL 15
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Best Local Similarity
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A;Molecule type: DNA
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RESULT 8 G83358

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Search completed: August 30, 2006, 04:30:51 Job time : 12.7273 secs
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                                                                                                                                                                                                                                                                                                                                        6 VDEQFPQHGL 15
A; Reference number: Z15740
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A; Status: preliminary
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A;Accession: S76407
A;Status: preliminary
A;Status: preliminary
A;Status: preliminary
A;Nole: L218 «KAN»
A;Cross-references: UNIPROT:P74435; UNIPARC:UPI0000137608; EMBL:D90915; GB:AB001339; NID
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Superfamily: phosphoribosylanthranilate isomerase; trpF homology
C;Keywords: intramolecular oxidoreductase; isomerase
F;6-210/Domain: trpF homology <TRF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pyruvate dehydrogenase (lipoamide) (EC 1.2.4.1) beta chain - garden pea C;Species: Pisum sativum (garden pea) C;Species: Disum sativum (garden pea) C;Accession: 106532 Wsequence_revision 23-Apr-1999 #text_change 12-Jul-2004 C;Accession: T06532 Whernyk, J.A.; Randall, D.D. Submitted to the EMBL Data Library, April 1996 A;Description: cDNA encoding the Pisum sativum mitochondrial pyruvate dehydrogenase Elbé
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-271 (WIL)
A;Cross-references: UNIPROT:062225; UNIPARC:UPI0000079A2B; EMBL:Z81528; PIDN:CAB04283.1;
A;Experimental source: clone F35E2
                                                                                                                            phosphoribosylanthranilate isomerase (BC 5.3.1.24) - Synechocystis sp. (strain PCC 6803) C; Species: Synechocystis sp. A; Variety: PCC 6803 C; Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                           A, Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                    C;Accession: S76407
K;Kaneko, T.; Stco, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
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Pred. No. 17;
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A;Accession: T21777
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
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0; Mismatches
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80.0%;
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     118 IQGEKTVEQFPQ 129
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Best Local Similarity 80.0
Matches 8; Conservative
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tes 7; Conserva
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A,Gene: CESP:F35E2.2
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Best Local S
Matches 7
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                                                                              RESULT 12
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A;Accession: T06532
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-359 < LUE>
A;Residues: 1-359 < LUE>
A;Cross-references: UNIPROT:P52904; UNIPARC:UDI0000130C28; EMBL:U56697; NID:gl336096; PI
C;Superfamily: pyruvate dehydrogenase, El component, beta subunit
C;Keywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Synechocystis sp.
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 15-Mar-2004
C;Accession: 835157; 876243
R;Reddy, A.S.; Nuccio, M.L.; Gross, L.M.; Thomas, T.L.
B;Ant Mol. Biol. 22, 293-300, 1993
A;Title: Isolation of a Delta(6)-desaturase gene from the cyanobacterium Synechocystis s A;Reference number: 835157; MUID:93283633; PMID:8389613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A, Residues: 1-559 <RED>
A, Residues: USS SED>
A, Cross-references: UNIPARC:UPI0000032FF9; GB:L11421; NID:g349562; PIDN:AAA27286.1; PID: A, Cross-references: UNIPARC:UPI000032FF9; GB:L11421; NID:g349562; PIDN:AAA27286.1; PID: B; Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996
A,Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
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A;Experimental source: PCC 6803
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Superfamily: fatty acid desaturase/sphingolipid desaturase
C;Keywords: oxidoreductase; unsaturated fatty acid biosynthesis
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                                                                                                                                                                                                                                                                                                                                              Query Match 43.8%; Score 42; DB 2; Best Local Similarity 70.0%; Pred. No. 29; Matches 7; Conservative 2; Mismatches
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Pred. No. 29;
4; Mismatches
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Best Local Similarity 46.7%;
Matches 7; Conservative
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Q2pytO physoderma Q7kyy7 drosophila Q9vxll drosophila Q4gza8 trypanosoma P22579 saccharomyc Q3ckr9 thermoanaer Q65wbl mannheimia Q6tku8 escherichia Q6tku8 escherichia Q36pa4 marinobacte Q6abdy prophonibac Q2ikul anaeromyxob Q7n997 photorhabdu

protein

Run on:

Sequence:

Minimum DB Maximum DB

Database

Result

Searched:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=16311624; DOT=10.1371/journal.pgen.0010665; Wu M., Ren Q., Durkin A.S., Daugherty S.C., Brinkac L.M., Dodson R.J., Madupu R., Sullivan S.A., Kolonay J.F., Nelson W.C., Tallon L.J., Jones K.M., Ulrich L.E., Gonzalez J.M., Zhulin I.B., Robb F.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria, Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Xenorhabdus.
NCBL_TaxID=40576;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Carboxydothermus hydrogenoformans (strain Z-2901 / DSM 6008).
Bacteria, Firmicutes, Clostridia; Clostridiales, Peptococcaceae;
Carboxydothermus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Life in hot carbon monoxide: the complete genome sequence of Carboxydothermus hydrogenoformans Z-2901."; PLoS Genet. 1:563-574 (2005).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             / 2581; -.
proteome; Hypothetical protein.
245 AA; 27478 MW; 246C9Fb7B62C318D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58.3%; Score 56; DB 2; ilarity 44.4%; Pred. No. 1.3; Conservative 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                 22-NOV-2005, integrated into UniProtKB/TrEMBL. 22-NOV-2005, sequence version 1. 07-FBE-2006, entry version 3. 07-FBE-2006, entry version 3. OrderedLocusNames=CHY_2581;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
                                                                                                                                                                                                                                                                                                                                      245 AA
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TIGR; CHY 2581; -.
                          Q9VXLI DROME
Q4GZA8 9TRYP
SIN3 YEAST
Q8DKM9 SYNEL
                                                                                                                                                                                                                                                       ALIGNMENTS
                                                                                                                                                                    Q6ABQ0 PROAC
Q2IKU1 9DELT
Q7N9G7 PHOLL
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MANSM
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ECOLI
MARHY
                                                                                          Q3CKR9_
Q65WB1_
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07N9G7
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01-MAR-2002, sequence version 1.
07-FBB-2006, entry version 17.
Peptide synthetase XpsA.
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VDGELIEQNFEQHGISKQ 192
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Xenorhabdus bovienii.
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Best Local Similarity
Local 8; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=246194;
VE9 XENBV
QBVQF9 XENBV 1
QBVQF9;
                                                                                                                                                                                                                                                                                                                                    Q3A910_CARHZ
Q3A910;
 Complete ; SEQUENCE
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yersinia ps
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drosophila
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Q8vqf9 xenorhabdus
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caenorhabdi
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bordetella
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                                                                                                         August 30, 2006, 04:22:32 ; Search time 70.1818 Seconds (without alignments) 237.245 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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0450w0
0981mx1
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033268
08.716
061777
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03iw14
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08clw8
0664y3
0681c8
075bz8
037vc6
05kyi0
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                GenCore version 5.1.9 (c) 1993 - 2006 Biocceleration Ltd
                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                       2849598 seqs, 925015592 residues
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Q8X7U6_ECO57
Q61Y77_CAEBR
Q43G89_9CHLB
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074BV7 GEOSL
07CTJ2 AGRT5
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Q5KYI0_GEOKA
Q9GZ15_DROME
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Q8VQF9 XENBV
Q5GR68 ALCXX
Q450W0 9BURK
Q4LMX1 9BURK
Q8BRC3 PSEPK
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BORPA
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Q99PU5_MOUSE
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Q3PQW7_NITHA
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Maximum Match 100%
Listing first 45 summaries
                                                                              - protein search, using sw model
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                                                                                                                                                                                                       1 IDGQKVDEQFPQHGLVKQ 18
                                                                                                                                                                                                                                                      Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
                                                                                                                                                                                                                                                                                                                                                       seq length: 0
seq length: 200000000
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96
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Match
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Perfect score:
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Gaps

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Length 245; Indels

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1008 AA; 114817 MW; A9F92682878061E5 CRC64;
                                                                                                     516 VDGLKQLLTETAEKVDEEFPQH 537
                                                                                 1 IDG------QKVDEQFPQH 13
                                                                                                                                                                   PRT;
                                                                                                                                                                                                      13-SEP-2005, sequence version 1. 21-FEB-2006, entry version 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 IDGQKVDEQFPQHGLVKQ 18
                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00005; ABC tran; 1.
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                                          Local Similarity 45.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR01415; ANKYRIN
                                                                                                                                                                                                                                        ORFNames=BcenDRAFT_2623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  preliminary data.
                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                         NCBI_TaxID=331271;
                                                                                                                                                                                                                              ABC transporter
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          SEQUENCE
                                   Query Match
Plasmid.
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                                                                     Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Paces V.;
                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alcaligenes xylosoxydans xylosoxydans (Achromobacter xylosoxidans).
Plasmid pA81.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jencova V., Strnad H., Chodora Z., Ulbrich P., Hickey W.J., Paces "Chlorocatechol catabolic enzymes from Achromobacter xylosoxidans
                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Alcaligenaceae; Achromobacter.
                                                                                                                                                                                                                                                                                                                                     53.1%; Score 51; DB 2; Length 1089; 52:9%; Pred. No. 40; ive 2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                    PROSITE; PS50075; ACP DOWAIN; 1.
PROSITE; PS00455; AMP_BINDING; 1.
SEQUENCE 1089 AA; 122987 MW; FF42CIA12506CBF9 CRC64;
                      STRAIN=T228;
Pinyon R.A., Thomas C.J.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jencova V.;
Submitted (JAN-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biodeterior. Biodegradation 54:175-181 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2005, integrated into UniProtKB/TrEMBL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AJ515144; CAI47903.1; -; Genomic_DNA. GO; GO:0003677; F:DNA binding; IEA. GO; GO:0004803; F:transposase activity; IEA. GO; GO:0006313; P:DNA transposation; IEA. DifferPro; IPR002513; Transposase_7. Pfam; PF01526; Transposase_7; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 1008 A.A.
                                                                                                                           GO; GO:0048037; Frofactor binding; IEA.
GO; GO:0016874; F:1igase activity; IEA.
GO; GO:001152; P:metabolism; IEA.
InterPro; IPR010071; AA adenyl dom.
InterPro; IPR000813; AWP-bind.
InterPro; IPR00133; AWP-bind.
InterPro; IPR001342; Condensath.
InterPro; IPR001543; Pisphopanteth bd.
Pfam; PF00501; AMP-binding; 1.
Pfam; PF005501; P-binding; 1.
PRINTS; PR00154; AMPBINDING.
TIGREAMS; TIGR01733; AA-adenyl-dom; 1.
                                                                                                       EMBL; AF455810; AAL57599.1; -; Genomic_DNA
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QSGR68;
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tes 9; Conservative
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           NUCLEOTIDE SEQUENCE
                                                                                                                      P14687; 1AMU.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=AU 1054;
US DOE Joint Genome Institute (JGI-PGF);
Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
Hammon N., Israni S., Pitluck S., Richardson P.;
"Sequencing of the draft genome assembly of Burkholderia cenocepacia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=AU 1054;
US DOOB Joint Genome Institute (JGI-ORNL);
Larimer F., Land M.;
"Annotation of the draft genome assembly of Burkholderia cenocepacia
                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales,
Burkholderiaceae, Burkholderia, Burkholderia cepacia complex.
   DB 2; Length 1008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 271;
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                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Probom; PD000006; ABC transporter; 1.
SMART; SM00382; AAA; 1.
PROSITE; PS00211; ABC TRANSPORTER 1; 1.
PROSITE; PS00893; ABC TRANSPORTER 2; 1.
SEQUENCE 271 AA; 25686 MW; E9976DF676E02527 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:0016020; C:membrane; IEA.
GO; GO:0018866; C:organelle inner membrane; IEA.
GO; GO:0018867; F:ATP binding; IEA.
GO; GO:00016887; F:ATPase activity; IEA.
GO; GO:000166; F:nucleotide binding; IEA.
GO; GO:0008810; P:transport; IEA.
InterPro; IPR003593; AAA ATPase.
InterPro; IPR003499; ABC_transp_like.
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                                                                                                                                                                                                                                                                                                                                                                                                                13-SEP-2005, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                           271 AA.
52.6%; Score 50.5; I
45.5%; Pred. No. 45;
iive 3; Mismatches
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Larimer F., Land M.;
"Annotation of the draft genome assembly of Burkholderia cenocepacia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                      Hammon N., Israni S., Pitluck S., Richardson P.,
"Sequencing of the draft genome assembly of Burkholderia cenocepacia
                                                                                                                                                                                                                                     US DOB Joint Genome Institute (JGI-PGF);
Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
Hammon N., Israni S., Pitluck S., Richardson P.;
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                                                                                                                                            Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales,
Burkholderiaceae, Burkholderia, Burkholderia cepacia complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 271;
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                                                                                                                                                                                                                                                                                                                    Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00382; AAA; 1.
PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
GROHENCE 271 AA; 29686 MW; E9976DF676E02527 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AAHLO1000041; EAW17437.1; -; Genomic_DNA. GO; GO:0016020; C:membrane; IEA. GO; GO:0016020; C:membrane; IEA. GO; GO:001686; C:organelle inner membrane; IEA. GO; GO:001687; F:ATP binding; IEA. GO; GO:001687; F:ATP binding; IEA. GO; GO:000166; F:nucleotide binding; IEA. GO; GO:000810; P:transport; IEA. InterPro; IPR003593; AAA ATPase. InterPro; IPR003439; ABC_transp_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 50; DB 2;
Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OBERC3 PSEPK PRELIMINARY; PRT; 283 AA. 088RC3; integrated into UniProtKB/TrEMBL. 01-JUN-2003; sequence version 1.
                                               integrated into UniProtKB/TrEMBL
                271 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Prints, Process, ABC tran; 1.
PRINTS; PRO1415; ANKYRIN.
Probom; PD00006; ABC transporter; 1.
                PRT;
                                                         02-AUG-2005, sequence version 1.
21-FEB-2006, entry version 7.
                                                                                                                           Burkholderia cenocepacia HI2424.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VDGERVDRPHPDRGLVFQ 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52.1%;
50.0%;
                PRELIMINARY;
                                                                                                           ORFNames=Bcen2424DRAFT_2386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    preliminary data.
                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                        NCBI_TaxID=331272;
                                                                                            ABC transporter
                                                                                                                                                                                                                          STRAIN=HI2424;
                                                                                                                                                                                                                                                                                                                                                                    STRAIN=HI2424;
              Q4LMX1_9BURK
Q4LMX1;
                                              02-AUG-2005,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6
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   9BURK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q88RC3
ID Q8
AC Q8
DT 01
DT 01
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PUDMOG=16111624; DOI=10.1371/journal.pgen.0010065;
Wu M., Ren Q., Durkin A.S., Daugherty S.C., Brinkac L.M., Dodson R.J.,
Madupu R., Sullivan S.A., Kolonay J.F., Nelson W.C., Tallon L.J.,
                                                                                                                                                                                                                                                                            MEDLINE=22423060; PubMed=12534461;
DOI=10.1046/j.1462-2920.2002.00366.x;
Nolson K.E., Wainel C., Paulsen I.T., Dodson R.J., Hilbert H.,
Nartins dos Santcs V.A.P., Foute D.E., Gill S.R., Pop M., Holmes M.,
Brinkac L.M., Beanan M.J., DeBoy R.T., Daugherty S.C., Kolonay J.F.,
Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M.,
Hance I., Chris Lee P., Holtzapple E.K., Scanlan D., Tran K.,
Wedler H., Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S.
Kiewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Tuemmler B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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OrderedLocusNames=CHY 0057;
Carboxydochtermus hydrogenoformans (strain Z-2901 / DSM 6008).
Bacteria; Firmicutes; Clostridia; Clostridiales; Peptococcaceae;
Carboxydothermus.
                                                                                        Pseudomonas putida (strain KT2440).

Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales,
Pseudomonadaceae; Pseudomonas.

NCBI_TaxID=160488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Complete genome seguence and comparative analysis of the
21-FEB-2006, entry version 23.
Nitrate ABC transporter, ATP-binding protein, putative.
OrderedLocusNames=PP0209; ORFNames=PP_0209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       metabolically versatile Pseudomonas putida KT2440.";
Environ. Microbiol. 4:799-808(2002).
-!- SIMILARITY: Belongs to the ABC transporter family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATP-binding, Complete proteome; Nucleotide-binding, Tr. SEQUENCE 283 Aa; 31651 MW; DAIB21FCA2223A4A CRC64;
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PROSITE; PS00211; ABC TRANSPORTER_1; UNKNOWN_1.
PROSITE; PS50893; ABC TRANSPORTER_2; 1.
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                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
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GO; GO:0016887; F:ATPase activity; IEA.
GO; GO:0000166; F:nuclectide binding; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IPR003593; AAA ATPase.
InterPro; IPR003439; ABC_transp_like.
Pfam; PF00005; ABC_tran; 1.
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ProDom; PD000006; ABC transporter; 1.
ProDom; AAA; 1.
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les 10; Conservative
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Q3AG05;
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Matches
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                                                                                                                                                                                                                                                    Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete proteome, Hydrolase, Membrane, Protease, Serine protease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OrderedLocusNames=SSO 0250; ORFNames=SSO_0250; Shigella a sonnei (strain SSO46).
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7
Jones K.M., Ulrich L.E., Gonzalez J.M., Zhulin I.B., Robb F.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                  "Life in hot carbon monoxide: the complete genome sequence of Carboxydothermus hydrogenoformans Z-2901.";
PLoS Genet. 1:563-574 (2005).
-i. SIMILARITY: Contains I PDZ (DHR) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51.0%; Score 49; DB 2; Length 616; 50.0%; Pred. No. 48; ive 6; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                             IIGR; CHY 0057; ...
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0008233; F:peptidase activity; IEA.
GO; GO:000525; F:protein binding; IEA.
GO; GO:0004252; F:serine-type endopeptidase activity; IEA.
GO; GO:0006508; P:proteolysis; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 49; DB 2; Length 370;
Pred. No. 28;
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SEQUENCE 616 AA; 71178 MW; 1C4B9A3B0CE75306 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        370 AA; 39702 MW; B512C002579F1384 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0250; ORFNames=SSO_0250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-SEP-2005, integrated into UniProtKB/TrEMBL
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5; Mismatches
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InterPro; IPR010272; DUF879_bac.
Pfam; PF05947; DUF879; 1.
                                                                                                                                                                                                                                                                                                                                                                EMBL; CP000141; ABB15592.1; -; Genomic_DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic Acids Res. 33:6445-6458(2005).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-SEP-2005, sequence version 1. 07-FEB-2006, entry version 5. Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |:|| :||:| :||
277 IEGQTIDEEFAQYKGLKQ 294
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50.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 50.0.
Best Acad 9; Conservative
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Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transmembrane
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Q3Z5C8;
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Distributed under the Creative Commons Attribution-Noberivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

STRAIN=0157:H7 / Sakai / RIMD 0509952 / EHBC;

MEDLINE=21156231; PubMed=11258796; DOI=10.1093/dnares/8.1.11;

Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,

Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,

Tida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,

Kuhara S., Shiba T., Hattori M., Shinagawa H.;

"Complete genome sequence of enterohemorrhagic Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Perna N.T., Plunkett G. III, Burland V. Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.;
"Genome sequence of enterchaemorrhagic Escherichia coli O157:H7.";
Nature 409:529-533(2001).
                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0157:H7 and genomic comparison with a laboratory strain K-12.";
DNA Res. 8:11-22(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
STRAIN=0157:H7 / EDL933 / ATCC 700927 / EHEC;
MEDLINE=21074935; PubMed=11206551; DOI=10.1038/35054089;
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QBXTU6 ECOS7 PRELIMINARY; PRT; 616 AA.
QBXTU6; Q7AHI7;
01-MAR-2002, integrated into UniProtKB/TrEMBL.
01-MAR-2005, sequence version 1.
01-MAR-2006, entry version 22.
No significant matches (Hypothetical protein EC80229)
OrderedLocusNames=EC90229, 20260;
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EMBL, BA0000007; BAB33652.1; -; Genomic_DNA.
PIR; E85509; E85508.
PIR; E90657; E90657.
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58 QKIEDEFPELTHGLIK 73
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Matches 8; Conserv
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Q61Y77_CAEBR
Q61Y77;
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QZJEG1_9ACTO
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Q47YD9;
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US DOB Joint Genome Institute (JGI-PGF);
Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T., Hammon N., Israni S., Pitluck S., Richardson P.;
"Sequencing of the draft genome and assembly of Chlorobium
                                     Dibmed=14624247; DOI=10.1371/journal.pbio.0000045;
Stein L.D., Bao Z., Blasiar D., Blumenthal T., Brent M.R., Chen N.,
Chinwalla A., Clarke L., Clee C., Coghlan A., Coulson A.,
Griffiths-Jones S., Harris T.W., Hillier L.W., Kamath R.,
Kuwabara P.B., Mardis B.R., Marra M.A., Miner T.L., Minx P.,
Mullikin J.C., Plumb R.W., Rogers J., Schein J.E., Sohrmann M.,
Waterston R.H.;
                                                                                                                                                                                                                                                                                            Natoria Garangero., 'Blod. 1:166-11:166-12003).
CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                             "The genome sequence of Caenorhabditis briggsae: a platform for comparative genomics.";
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Chlorobium phaeobacteroides DSM 266.
Bacteria, Chlorobi, Chlorobia, Chlorobiales, Chlorobiaceae;
Chlorobium/Pelodictyon group; Chlorobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Length 345;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; CAACO1000016; CAEG0129.1; -; Genomic_DNA.
GO; GO:0004252; F:serine-type endopeptidase activity; IEA.
GO; GO:0006508; P:proteolysis; IEA.
InterPro; IPRO013154; Peptidase_S1_S6.
InterPro; IPRO01314; Peptidase_S1_S6.
PFo0089; Trypsin; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
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Similar to Uncharacterized protein conserved in bacteria.
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"Annotation of the draft genome assembly of Chlorobium phaeobacteroides DSM 266.";
Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.--- CAUTION: The sequence shown here is derived from an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      phaeobacteroides DSM 266. \ddot{n}_i Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PRO0722; CHYMOTRYPSIN.
SMART; SM00020; Tryp SPc; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
Complete proteome; Hypothetical protein.
SEQUENCE 345 AA; 38450 MW; 744C79ED3DB0408D CRC64;
SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-SEP-2005, integrated into UniProtKB/TrEMBL
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50.0%; Pred. No. 38;
ive 5; Mismatches
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Best Local Similarity 50.0
Matches 7; Conservative
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Q43G89_9CHLB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T., Hammon N., Israni S., Pitluck S., Golteman E., Martinez M., Schmutz J., Larimer F., Land M., Kyrpides N., Lykidis A., Francino P., Benson D.R., Huang Y., Mastronunzio J., Bickhart D., Niemann J., Rawnaley T., Tisa L.S., Richardson P., "Complete sequence of Frankia sp. Cc13"; Summitted (JAN-2006) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                           Gaps
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EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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11-SEP-2005, sequence version 1.
07-FEB-2006, entry version 3.
Efflux transporter, RND family, MFP subunit subfamily.
Order-edLocusNames-CPS_3507;
Colwellia psychrerythraea (strain 34H / ATCC BAA-681) (vibrio psychroerythus).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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                                                                                                                                                                                                                                                                                     DB 2; Length 442; 49;
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                                                                                                                                                               InterPro; IPR003006; Ig_MHC.
Pfam; PF05990; DUF900; 1.
PROSITE; PS00290; IG MHC.
SEQUENCE 442 AA; 48627 MW; 4877E0BFF60B46FC CRC64;
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SEQUENCE 851 AA; 92384 MW; B4197D33CA0FD261 CRC64;
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                                                                                                                                             EMBL; AAIB01000015; EAM34597.1; -; Genomic_DNA.
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                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                     50.0%; Score 48; 64.3%; Pred. No.
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NCBI_TaxID=106370;
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US DOE Joint Genome Institute;
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                                                                                                                                                                                                                                                                                                                                        9; Conservative
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                           preliminary data.
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Matches 9; Conserv
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Copeland A., Iucas S., Lapidus A., Barry K., Detter J.C., Glavina T.,

Hammon N., Israni S., Pitluck S., Martinez M., Schmutz J., Larimer F.,

Land M., Kyrpides N., Ivanova N., Richardson P.;

"Complete sequence of Synechococcus sp. CC9902.";

Submitted (AUG-2005) to the EMBL/GenBank/DDBJ databases.
                                            NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
PubMed=16043709; DOI=10.1073/pnas.0504766102;
Methe B.A., Nelson K.E., Deming J.W., Momen B., Melamud E., Zhang X., Mouth J., Madupu R., Nelson W.C., Dodson R.J., Brinkac L.M., Daugherty S.C., Durkin A.S., DeBoy R.T., Kolonay J.F., Sullivan S.A., Zhou L., Davidsen T.W., Wu M., Huston A.L., Lewis M., Weaver B., "The psychrophilic lifestyle as revealed by the genome sequence of Colwellia psychrerythraea 34H through genomic and protecomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gарв
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO:0005737; C:cytoplasm; IEA.
GO:0008792; F:arginine decarboxylase activity; IEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 471 AA; 51718 MW; C9DAA2CAEC3399BD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                              421 AA; 47005 MW; 89A1E9649C763790 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORFWames=Syncc9902 1380;
Synechococcus sp. [strain CC9902].
Bacteria; Cyanobacteria; Chrococcales; Synechococcus.
                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 102:10913-10918(2005).
                                                                                                                                                                                                                                                                                                                         R; CPS 3507; -. Go. Ool6020; C:membrane; IEA. GO:0016020; C:membrane; IEA. GO:0008565; F:protein transporter activity; IEA. GO:0009306; P:protein secretion; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-NOV-2005, integrated into UniProtKB/TrEMBL. 22-NOV-2005, sequence version 1. FEB-2006, entry version 3. Arginine decarboxylase (EC 4.1.1.19).
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GO:0006595; P:polyamine metabolism; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      471 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49.5%; Score 47.5; D
63.2%; Pred. No. 57;
tive 2; Mismatches
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                                                                                                                                                                                                                                                                                                           EMBL; CP000083; AAZ26956.1; -; Genomic_DNA
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TIGRFAMS; TIGR01730; RND_mfp; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 63.2
les 12; Conservative
Colwelliaceae; Colwellia.
NCBI_TaxID=167879;
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Best Local Similarity
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RX Pubmed-16/11072, DOI=10.1126/science.112014;

Rabded-16/11072; DOI=10.1126/science.112014;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
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MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
                                                                                                                                                                                                                                                     01-JUN-2001, sequence version 1.

01-JUN-2001, sequence version 1.

Lipidosis-related protein Lipidosin (2 days pregnant adult female coviduct cDNA, RIKEN Full-length enriched library, clone:E230019G03 product:lipidosis-related protein lipidosin, full insert sequence) (Gonadotrorpin-regulated long chain acyl CoA synthetase).

Name=Acsbg1; Synonyms=Lpd, lpd;

Mus musculus (Mouse).
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MEDLINE=20563802; PubMed=11112418; DOI=10.1006/bbrc.2000.3897;
                                                                                                                                                                                                                                  01-JUN-2001, integrated into UniProtKB/TrEMBL
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PubMed=16141072; DOI=10.1126/science.1112014;
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                                                322 LNGLEADEÓFMÓRGLIAE 339
1 IDGOKVDEQFPQHGLVKQ 18
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R. Hidd. S., Kannari-Kathama M., Santh M., And. 10, Arabara T.,
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C STRAIN=C57BL/6J; TISSTE=Oviduct;

MEDLINE=20530913; PubMed=11076661; DOI=10.1101/gr.152600;

MEDLINE=20530913; PubMed=11076661; DOI=10.1101/gr.152600;

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                                             STRAIN=C57BL/6J; TISSUE=Oviduct;
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Search completed: August 30, 2006, 04:29:09

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Sequence 25727, A Sequence 40, Appl Sequence 40, Appl Sequence 40, Appl Sequence 40, Appl Sequence 5222, Ap
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Sequence 5163, Ap
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: /EMC Celerra SIDS3/ptodata/2/iaa/H_COMB.pep:*
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GenCore version 5.1.9 . Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-09-487-558B-322
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                                               - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Sequence 19566, Application US/09248796A

Sequence 19566, Application US/09248796A

Sequence 19566, Application US/09248796A

Sequence 19566, Application US/09248796A

THIRD PROCEDURATION: WOUTLEIC AND THERAPEUTICS

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.132

CURRENT APPLICATION NUMBER: US/09/248,796A

CURRENT FILING DATE: 1999-02-12

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR APPLICATION NUMBER: US 60/074,726

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-06-13

SEQ ID NO 19566

LENGTH: 195
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Patent No. 6562958
CENERAL INFORMATION:
TITLE OF INVENTION: BADMANNII FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BADMANNII FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BADMANNII FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
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Sequence 23915, A
Sequence 2, Appli
Sequence 21451, A
Sequence 28, Appli
Sequence 28, Appli
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46399, A
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                                                                               Sequence
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Sequence
                              Sequence
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                        US-09-589-733C-18

US-09-580-713C-17

US-09-543-681A-8212

US-09-552-991A-25914

US-09-272-991A-30083

US-09-272-991A-30083

US-09-272-991A-21451

US-08-152-014A-21451

US-09-134-000C-6248

US-09-134-00C-6248

US-09-136-00C-6248

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2; Mismatches
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47.9%; Score 46;
Best Local Similarity 55.0%; Pred. No. Matches 11; Conservative 2; Mismatcl
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; ORGANISM: Acinetobacter baumannii
US-09-328-352-5163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Candida albicans
US-09-248-796A-19566
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441.7
441.1
441.1
440.6
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APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
                    Gaps
                                                                                                                                                                               Sequence 40, Application US/08961083

Patent No. 6159469

GENERAL INFORMATION:
APPLICANT: Choi et. al.
ITITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
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                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS version 6.2 SOFTWARE: ASCII Text
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Pred. No. 15;
Similarity 44.4%; Pred. No. 55; 8; Conservative 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                 STREET: 9410 Key West Avenue CITY: Rockville STATE: Marvi--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 40, Application US/09536784; Patent No. 6573082; GENERAL INFORMATION:
                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB
TELECOMMUNICATION INFORMATION:
                                                            18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43.8%;
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                                                            1 IDGQKVDEQFPQHGLVKQ
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INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 137 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93 iggekrveorpó 104
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
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Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                        Maryland: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 6
US-09-536-784-40
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JS-08-961-083-40
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                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: ARCHGINGSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ARCHGINGSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT PILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 25727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Silva, Jeff
APPLICANT: Summers, Bric
TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REPERENCE: 109272.130
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Query Match

46.9%; Score 45; DB 2; Length 1512;
Best Local Similarity 50.0%; Pred. No. 70;
Matches 8; Conservative 1; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46.9%; Score 45; DB 2; Length 1536; 53.3%; Pred. No. 71; tive 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44.8%; Score 43; DB 2; Length 612;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/487,558B CURRENT FILING DATE: 2000-01-19
                                                                                                                                                                                                                    Sequence 322, Application US/09487558B
Patent No. 6949356
GENERAL INFORMATION:
APPLICANT: Busby, Robert
APPLICANT: Cali, Brian
APPLICANT: Hedth, Perer
APPLICANT: Hedth, Perer
APPLICANT: Madden, Revin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-252-991A-25727
; Sequence 25727, Application US/09252991A
; Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/487,558 PRIOR FILING DATE: 1999-10-20 PUMBER OF SEQ ID NOS: 446 SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                     Maxon, Mary
Milne, Todd
No. 6949356man, Thea
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1370 IDGTEVDEEFSPEGI 1384
                                                                                                                      328 GDRTDPLMPSHGLVSQ 343
                                                                                 3 GOKVDEQFPQHGLVKQ 18
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Best Local Similarity 53.3
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               Royer, John
Salama, Sofie.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sherman, Amir
Silva, Jeff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-252-991A-25727
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 322
LENGTH: 1536
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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Sequence 40, Application US/09765272A

Patent No. 6929930
GENERAL INPORMATION:
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and
                                                                                                                                                                                                                                                                          43.8%; Score 42; DB 2; Length 137; 66.7%; Pred. No. 15; ive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: Dell Latitude C610
OPERATING SYSTEM: Windows 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sciences, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 08/961,083
FILING DATE: 0CT-30-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lin J. Hymel
REGISTRATION NUMBER: 45,414
REFERENCE/DOCKET NUMBER: PB340P2C2
TELECOMUNICATION INFORMATION:
TELEPHONE: (301) 610-5790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:

REPLICATION NUMBER: US/09/765,272A
FILING DATE: 22-Jan-2001
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 40:
                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 40:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSE: Human Genome Scien
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
                      1) 309-8504
309-8512
TELECOMMUNICATION INFORMATION
                    TELEPHONE: (301) 309-85C
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGHY: 137 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 137 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (301) 309-8439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single
                                                                                                                                            STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 66.7
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 IDGOKVDEQFPO 12
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Patent No. 6887665
GENERAL INFORMATION:
APPLICANT, Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
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                  ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/536,784
FILING DATE: 30-Oct-1997
CLASSIFICATION: -UNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/961,083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 42; DB 2; Length 137;
Pred. No. 15;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Human Genome Sciences, Inc
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
                                                                                                                                                                                                                                                                        FILING DATE: OCT-30-1997
ATTORNEY/AGENT INFORMATION:
NAME: MICHAELIE S. MARKE
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: FB340P3
TELECOMMUNICATION INFORMATION:
TELEPRAK: (301) 309-8512
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/765,271
FILING DATE: 22-Jan-2001
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/536,784
FILING DATE: «Unknown-
APPLICATION NUMBER: 08/961,083
FILING DATE: OCT-30-1997
ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: PB340P3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 40:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 137 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
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Best Local Similarity 66.7
Matches 8; Conservative
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US-09-765-271-40
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Sequence 6247, Application US/09134000C

| Sequence 6247, Application US/09134000C
| Patent No. 6617156
| GENERAL INFORMATION:
| APPLICANT: Lynn Doucette-Stamm et al APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO TITLE OF INVENTION: MUCHER: US/09/134,000C
| TITLE OF INVENTION: ENTERCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
| FILE REPERENCE: 032796-032
| CURRENT APPLICATION NUMBER: US/09/134,000C
| PRIOR FILING DATE: 1998-08-13
| PRIOR FILING DATE: 1997-08-15
| NUMBER OF SEQ ID NOS: 6812
| SEQ ID NO 6247
| LENGTH: 228
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                                                                                                                                                                                                                                                                                                                                                 Length 194;
                                                                                                                                                                                                                                                                                                                                                                                                 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08307382;
Patent No. 5552306;
GENERAL INFORMATION:
APPLICANT: Thomas, Terry L.
APPLICANT: Reddy, Avutu S.
APPLICANT: Reddy, Avutu S.
APPLICANT: Nuccio, Michael
APPLICANT: Preyssinet, Georges L.
TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC
TITLE OF INVENTION: ACID BY A DELTA 6-DESATURASE
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
                                                                                                                                                                                                                                                                                                                                                      7;
                                                                                                                                                                                         ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                      DB
22;
                                                                                                                                                                                                                    , NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...194
; SEQUENCE DESCRIPTION: SEQ ID NO: 5104:
US-09-107-433-5104
                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                      43.8%; Score 42; 66.7%; Pred. No.
INFORMATION FOR SEQ ID NO: 5104:
SEQUENCE CHRAACTERISTICS:
LIENGTH: 194 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Enterococcus faecalis
                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
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STATE: New York
COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 IQGEKTVEQFPQ 132
                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 66.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 IDGQKVDEQFPQ 12
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                                                                                                                                                                      ORIGINAL SOURCE:
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US-08-307-382-2
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                                                                                                                                                                           APPLICANT: Lynn Doucette-Stamm et al.
TILLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
FILE REFERENCE: PATHOD-07A
CURRENT APPLICATION NUMBER: US/09/583,110
CURRENT FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 99/107,433
PRIOR PLING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR FILING DATE: 1998-05-12
PRIOR FILING DATE: 1997-07-02
NUMBER OF SEQ ID NOS: 5322
LENGTH: 185
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; Patent No. 6800744
; GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: CD/ROM ISO9660
COMPUTER: CUNKNOWN>
COMPATING SYSTEM: CUNKNOWN>
SOFTWARE: CUNKNOWN>
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,433
FILING DATE: 30-Jun-1998
PRIOR APPLICATION NUMBER: 60/085131
FILING DATE: MAY 12, 1998
APPLICATION NUMBER: 60/051553
FILING DATE: July 2, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 42; DB 2
Pred. No. 21;
1; Mismatches
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NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-011
TELECOMMUNICATION INFORMATION:
                                                                                                                      Sequence 5222, Application US/09583110 Patent No. 6699703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT CAGANISM: Streptococcus pneumoniae US-09-583-110-5222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (781)893-50
TELEFAX: (781)893-8277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43.8%;
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Best Local Similarity 66.7,
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         93 IQGEKTVEQFPQ 104
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                                                                                                     US-09-583-110-5222
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Query Match
43.8%; Score 42; DB 1; Length 359;
Best Local Similarity 46.7%; Pred. No. 44;
Matches 7; Conservative 4; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:

ADDRESSE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City Plaza
CITY: United States
ZIP: 1153
ZIP: 1153
COMPUTER: IDM YOR:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,727
FILING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: US 08/307,382
FILING DATE: 14-SEP-1994
APPLICATION NUMBER: US 07/817,919
FILING DATE: 08-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: MCNULLY, WILLIAM E.
REFERENCE/DOCKET NUMBER: 8383Z
TELEPHONE: (516) 742-4343
TELEPHONE: (516) 742-4344
TELEPHONE: (516) 742-4346
TELERX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 2:
SEROMATION FOR SEQ ID NO: 2:
FUNCTH: TREEXTORMATION: TELEPHONE: TELEPHONE: TELESTORMATION: TELEPHONE: (516) 742-4343
TELERX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 2:
FUNCTH: TELEPHONE: TENETRICES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08478727;
Patent No. 5663068
GENERAL INFORMATION:
APPLICANT: Thomas, Terry L.
APPLICANT: Reddy, Avutu S.
APPLICANT: Reddy, Avutu S.
APPLICANT: Preyssinet, Georges L.
TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC
TITLE OF INVENTION: ACID BY A DELTA 6-DESATURASE
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                         Query Match
43.8%; Score 42; DB
Best Local Similarity 46.7%; Pred. No. 44;
Matches 7; Conservative 4; Mismatches
                                                                                                                                                                                                                                                                                                                          4 OKVDEQFPQHGLVKQ 18
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                                                                                    : 359 amino acids
amino acid
            TELEX: 230 901 SANS UR INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                  MOLECULE TYPE: protein US-08-366-779-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
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US-08-478-727-2
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; Sequence 2, Application US/08366779
; Patent No. 5614393
; GENERAL ITPORMATION:
    APPLICANT: Thomas, Terry L.
; APPLICANT: Reddy, Avutu S.
; APPLICANT: Nunberg, Michael
; APPLICANT: Nunberg, Andrew N.
; TITLE OF INVENTION: DELTA 6-DESATURASE
; NUMBER OF SEQUENCES:
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43.8%; Score 42; DB 1; Length 359; 46.7%; Pred. No. 44;
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COMPUTER: Patentin Pc-DoS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/307,382
FILING DATE: 14-SEP-1994
CLASSIFICATION NUMBER: US 07/817,919
FILING DATE: 08-JAN-1992
ATPORNEY/AGENT INFORMATION:
NAME: MACNULTY, William E.
REGISTRATION NUMBER: 22,666
REPERBUCK/DOCKET UNBER: 8383Z
TELECOMMUNICATION INFORMATION:
TELEFHONE: (516) 742-4366
TELEFRA: (516) 742-4366
TELEFRA: (516) 742-4366
TELEFRA: (516) 742-4366
TELEFRA: CASAMENTICS:
SEQUENCE CHARACTERICIS:
SEQUENCE CHARACTERICIS:
SEQUENCE CHARACTERICIS:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/366,779
FILING DATE: 30-DEC-1994
CLASSIFCATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Presser, Leopold
REGISTRATION NUMBER: 19,827
REFERENCE/DOCKET NUMBER: 93832YXW
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Scully, Scott, Murphy & Presser
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
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(516) 742-4366
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21 QRVDAYFAEHGLTQR 35
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amino acid
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COUNTRY: United States
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Best Local Similarity
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US-08-366-779-2
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Search completed: August 30, 2006, 04:33:00 Job time : 18.8182 secs

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Sequence 11, Appl
Sequence 2, Appli
Sequence 5, Appli
Sequence 14, Appli
Sequence 14630',
Sequence 14530',
Sequence 19596', A
Sequence 19596', A
Sequence 320', Appl
Sequence 36065', A
Sequence 16103',
Sequence 16103',
Sequence 16103',
Sequence 16103',
Sequence 1712', Appl
Sequence 1712', Appl
Sequence 1712', Appl
Sequence 1712', Appl
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Sequence 1712', Appl
Sequence 1712', Appl
Sequence 1713', Sequence 1713', Appl
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784, App
3776, Ap
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210792,
42340, A
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37611, A
39926, A
30, Appl
37769, A
                                                                                                                                                                                                                                                                                                                                                                                                     Published Applications AA Main:*

: /BMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

: /BMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

: /BMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

: /BMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

: /BMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

: /BMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
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                                                                           August 30, 2006, 04:33:28 , Search time 90.9091 Seconds (without alignments) 91.717 Million cell updates/sec
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Sequence
GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-10-451-078-2

US-10-451-078-4

US-10-051-078-4

US-10-214-524-30

US-10-224-529-146307

US-10-224-529-146307

US-10-244-599-146307

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US-10-450-763-36065

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US-10-437-963-154933

US-10-118-298-3776

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Listing first 45 summaries
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US-10-767-701-45372 US-10-767-701-45372 US-10-425-115-216179 US-10-767-701-42582 US-10-767-701-42582 US-10-425-114-40459 US-10-425-114-57633 US-10-425-114-67639 US-10-425-114-67344 US-10-425-114-67344 US-10-425-114-67344 US-10-424-599-157014 US-10-474-599-157014 US-10-474-776-661 US-10-474-776-661 US-10-672-928-1286	ALIGNMENTS SEGUET 1 S10-758-165-11 S10-758-165-11 GENEROL 11. Application US/10758165 Publication No. US20050196816A1 GENERAL INFORMATION: APPLICANT: Hammerberg, Bruce TITLE OF INVENTION: APPLICANT: Hammerberg, Bruce TITLE REPERENCE: 5051-661 CURRENT APPLICATION NUMBER: US/10/758,165 CURRENT APPLICATION NUMBER: US 60/440,472 PRIOR FILING DATE: 2004-01-16 RIOR FILING DATE: 2003-01-16 NUMBER OF SEQ ID NOS: 16 SOFTWARE: PATENTIN OF SIGN 3.2 SOFTWARE: PATENTIN OF SEQ ID NOS: 16 SOFTWARE: PATENTIN OF SEQ ID NOS: 16 SOFTWARE: PATENTIN OF SEQ ID NOS: 16 SOFTWARE: PATENTIN OF SEQ ID NOS: 16 SOFTWARE: PATENTIN OF SEQ ID NOS: 16 SOFTWARE: PATENTIN OF SEQ ID NOS: 16 SOFTWARE: PATENTIN OF SEQ ID NOS: 16 SOFTWARE: PATENTIN OF SEQ ID NOS: 16 SOFTWARE: PATENTIN OF SEQ ID NOS: 16 SOFTWARE: PATENTIN OF SEQ ID NOS: 16 SOFTWARE: PATENTIN OF SEQ ID NOS: 16 SOFTWARE: PATENTIN OF SEQ ID NOS: 16 SOFTWARE: PATENTIN OF SEQ ID NOS: 16 SOFTWARE: PATENTIN OF SEQ ID NOS: 16 SOFTWARE: PATENTIN OF SEQ ID NOS: 16 SOFTWARE: PATENTIN OF SEQ ID NOS: 16 SOFTWARE: PATENTIN OF SEQ ID NOS: 16 SOFTWARE: PATENTIN OF SEQ ID NOS: 16 SOFTWARE: PATENTIN OF SEQ ID NOS: 16 SOFTWARE: PATENTIN OF SEQ ID NOS: 16 SOFTWARE: PATENTIN OF SEQ ID NOS: 16 SOFTWARE: PATENTIN OF SEQ ID NOS: 16 SOFTWARE: PATENTIN OF SEQ ID NOS: 16 SOFTWARE: PATENTIN OF SEQ ID NOS: 16 SOFTWARE: PATENTIN OF SEQ ID NOS: 16 SOFTWARE: PATENTIN OF SEQ ID NOS: 16 SOFTWARE: PATENTIN OF SEQ ID NOS: 16 SOFTWARE: PATENTIN OF SEQ ID NOS: 16 SOFTWARE: PATENTIN OF SEQ ID NOS: 16 SOFTWARE: PATENTIN OF SEQ ID NOS: 16 SOFTWARE: PATENTIN OF SEQ ID NOS: 16 SOFTWARE: PATENTIN OF SEQ ID NOS: 16 SOFTWARE: PATENTIN OF SEQ ID NOS: 16 SOFTWARE: PATENTIN OF SEQ ID NOS: 16 SOFTWARE: PATENTIN OF SEQ ID NOS: 16 SOFTWARE: PATENTIN OF SEQ ID NOS: 16 SOFTWARE: PATENTIN OF SEQ ID NOS: 16 SOFTWARE: PATENTIN OF SEQ ID NOS: 16 SOFTWARE: PATENTIN OF SEQ ID NOS: 16 SOFTWARE: PATENTIN OF SEQ ID NOS: 16 SOFTWARE: PATENTIN OF SEQ ID NOS: 16 SOFTWARE: PATENTIN OF SEQ ID NO	Score 96; DB 5; Length Pred. No. 9.4e-09; Mismatches 0; Indel 8	eic Acids which Encode tof an Equine IgE Allotygins Obtained Using Themific Monoclonal Antibodi 7451,078
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Sequence 30, Application US/10214524

Sequence 30, Application US/10214524

Publication No. US20030073142A1

GENERAL INFORMATION:

APPLICANT: Chen, Swey-Shen Alex

APPLICANT: Wang, Yong-Min

APPLICANT: Barankiewicz, Theresa J.

APPLICANT: Chen, Zhong

APPLICANT: Chen, Zhong

TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF

FILE REFERENCE: IGE-00101.P.1.1

CURRENT APPLICATION NUMBER: US/10/214,524

CURRENT FILING DATE: 2002-08-08

PRIOR FILING DATE: 2001-08-13

NUMBER OF SEQ ID NOS: 61

SEQ ID NO 30

LENGTH: 569
                                                                                                                                                                                                                                                                     Sequence 5, Application US/10052788

Sequence 5, Application US/10052788

Publication No. US20030087314A1

GENERAL INFORMATION:
APPLICANT: Gerbind, Howard David
APPLICANT: Fettigrew, Howard David
APPLICANT: The Regents of the University of California
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Epsilon Immunoglobulin Chain Derived Peptides for
TITLE OF INVENTION: Induction of Anti-IgE Antibodies
FILE REFERENCE: 023070-121000US
CURRENT APPLICATION NUMBER: US/10/052,788

CURRENT FILING DATE: 2001-11-08

NUMBER OF SEQ ID NOS: 6

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 5.

LEAGTH: 15
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81.2%; Score 78; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.4e-06;
Matches 14; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 3.2e-07;
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; ORGANISM: Horse (Equus caballus)
US-10-214-524-30
                                                                                                                                                             145 IDGQKVDEQFPQHGLVKQ 162
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                    Query Match
Best Local Similarity 100.0
Matches 18; Conservative
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Sequence 4, Application US/10451078

Publication No. US20040115764A1

GENERAL INFORMATION:

APPLICANT: Leibold, Wolfgang

APPLICANT: Bacthra, Wagner

APPLICANT: Radbruch, Andreas

TITLE OF INVENTION: Heavy Chain of an Equine IgE Allotype, Recombinant

TITLE OF INVENTION: Immunoglobulins Obtained Using Them, and Corresponding

TITLE OF INVENTION: Immunoglobulins Obtained Using Them, and Corresponding

TITLE OF INVENTION: Isotype-specific Monoclonal Antibodies and their Use

FILE REFERENCE: 03100177aa

CURRENT APPLICATION NUMBER: US/10/451,078

CURRENT APPLICATION NUMBER: DET/DE01/04810

PRIOR FILING DATE: 2001-12-20

PRIOR FILING DATE: 2001-12-21

NUMBER OF SEQ ID NOS: 7

SOFTWARE: PatentIn version 3.2

SEQ ID NO 4

LENGTH: 424
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100.0%; Pred. No. 3.2e-07;
tive 0; Mismatches 0; Indels
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NAME/KEY: Domain
NAME/KEY: Domain
OTHER INFORMATION: (1). (97)
OTHER INFORMATION: CHI domain, IGE allotype a
                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (313)..(424)
CTHER INFORMATION: CH4 domain, IGE allotype a
US-10-451-078-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Domain
LOCATION: (98)..(205)
OTHER INFORMATION: CH2 domain, IGE allotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (1)..(97)
OTHER INFORMATION: CH1 domain, IgE allotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (206)..(312)
OTHER INFORMATION: CH3 domain, IGE allotype
                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KGN: Domain
LOCAT/KGN: (206)..(312)
OTHER INFORMATION: CH3 domain, IGE allotype
                                                                                                                                                                                                                                              LOCATION: (98)..(205)
OTHER INFORMATION: CH2 domain, IgE allotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             145 IDGQKVDEQFPQHGLVKQ 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0
Matches 18; Conservative
                                                  TYPE: PRT
ORGANISM: Equus caballus
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NAME/KEY: Domain
LOCATION: (98)..(2
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NAME/KEY: Domain
LOCATION: (206)..
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NAME/KEY: Domain
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; SEQ ID NO 2
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GENERAL INFORMATION:
APPLICANT: Venter, J. Craig
APPLICANT: Venter, J. Craig
APPLICANT: Venter, J. Craig
APPLICANT: Venter, J. Craig
APPLICANT: et al.
TITLE OF INVENTION: DETECTING EXPRESSION OF 10,000 OR MORE
TITLE OF INVENTION: DROSOPHILA GENES.
TITLE OF INVENTION: DROSOPHILA GENES.
TITLE OF INVENTION: DROSOPHILA GENES.
CURRENT APPLICATION NUMBER: US/11/097,143
CURRENT APPLICATION NUMBER: 60/157,832
PRIOR PELLING DATE: 1999-10-19
PRIOR PILING DATE: 1999-10-28
PRIOR PELLING DATE: 1999-10-28
PRIOR PELLING DATE: 1999-10-28
PRIOR PELLING DATE: 1999-11-2-8
PRIOR PELLING DATE: 1999-11-2-8
PRIOR PELLING DATE: 1999-11-2-8
PRIOR FILING DATE: 1999-11-2-8
PRIOR FILING DATE: 1999-11-3
PRIOR FILING DATE: 2000-01-12
PRIOR APPLICATION NUMBER: 60/173,383
PRIOR FILING DATE: 2000-01-12
PRIOR APPLICATION NUMBER: 60/194,831
PRIOR FILING DATE: 2000-01-2
PRIOR APPLICATION NUMBER: 60/194,831
PRIOR FILING DATE: 2000-03-24
PRIOR APPLICATION NUMBER: 60/194,831
PRIOR FILING DATE: 2000-03-24
PRIOR PELLING DATE: 2000-03-24
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PRIOR PELLI
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PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 55836
LENGTH: 504
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53.3%; Pred. No. 1.5e+02;
cive 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 19596, Application US/11097143
Publication No. US20050208558A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                        ORGANISM: Enterobacter cloacae
US-10-282-122A-55836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        315 ibgervbiokpahai 329
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Best Local Similarity 53.3.
Thes 8; Conservative
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Best Local Similarity
Matches 8; Conserva
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US-09-801-368-322
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                                                                                                                                                                              Sequence 146307, Application US/10424599

Fublication No. US20040031072A1

GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILLE REPRENCE: 38-21 (5123.8)
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 146307
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FILE REPERENCE: ELITRA.034.022,122A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR PLING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-66
PRIOR PILING DATE: 2000-05-66
PRIOR PILING DATE: 2000-05-67
PRIOR FILING DATE: 2000-05-09
PRIOR PILING DATE: 2000-05-09
PRIOR PILING DATE: 2000-05-09
PRIOR PILING DATE: 2000-05-09
PRIOR PILING DATE: 2000-05-09
PRIOR PILING DATE: 2000-05-33
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-110-23
PRIOR PILING DATE: 2000-110-23
PRIOR PILING DATE: 2000-110-23
PRIOR PILING DATE: 2000-110-23
PRIOR PILING DATE: 2000-110-27
PRIOR PILING DATE: 2000-112-22
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US-10-424-599-146307
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Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Haselbeck, Robert
APPLICANT: Wall, Paniel
APPLICANT: Tawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
          291 IEGQKVDEQFPTQASMKQ 308
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Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 IDGOKVDEOFPOHG 14
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Matches 8; Conservative
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ORGANISM: Glycine max
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US-10-282-122A-55836
                                                                                                                                               RESULT 6
US-10-424-599-146307
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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Expensive David K
APPLICANT: Show Yihua
APPLICANT: The Vinua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 39-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 145103
LENGTH: 130
                                                                                                    GENERAL INVACATALON:

GENERAL INVACATALON:

TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

FILE REPERENCE: 790CIP3/US

CURRENT APPLICATION NUMBER: US/10/450,763

CURRENT FILING DATE: 2003-06-11

PRIOR APPLICATION NUMBER: PCT/US01/08631

PRIOR FILING DATE: 20001-03-30

PRIOR APPLICATION NUMBER: 09/540,217

PRIOR PILING DATE: 2000-03-31

PRIOR PILING DATE: 2000-08-23

NUMBER OF SEQ ID NOS: 60736

SOFTWARE: CUSCOM

SEQ ID NOS: 60736

SEQ ID NOS: 60736

LENGTH: 128
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US-10-424-599-145103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature

: LOCATION: (1)...(128)

: OTHER INFORMATION: Xaa = X or * as defined in Table 2

US-10-450-763-36065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45.8%; Score 44; DB 5; 52.9%; Pred. No. 35;
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Pred. No. 36;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Mismatches
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Publication No. US20040031072A1
GENERAL INFORMATION:
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US-10-450-763-36064
; Sequence 36064, Application US/10450763
                                           Sequence 36065, Application US/10450763
Publication No. US20050196754A1
GENERAL INFORMATION:
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Best Local Similarity 69.2%;
Matches 9; Conservative
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Best Local Similarity 52.94
Matches 9; Conservative
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RESULT 11
US-10-450-763-36065
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Publication No. US20040031872A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
SEQ ID NO 205669
ILENGTH: 89
                                                                                                                                                                                                    APPLICANT: Stateman, Anire
APPLICANT: Stateman, Anire
APPLICANT: Silva, Jeff
APPLICANT: Silva, Jeff
APPLICANT: Silva, Jeff
APPLICANT: Summers, Exic
TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFERENCE: 109272.147
CURRENT APPLICATION NUMBER: US,09/801,368
CURRENT PILING DATE: 2000-03-07
PRIOR FILING DATE: 2000-01-19
PRIOR FILING DATE: 1099-10-20
NUMBER OF SEQ ID NOS: 440
SEQ ID NOS: 440
SEQ ID NO 322
LENGTH: 1536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 45; DB 3; Length 153
Pred. No. 3.8e+02;
3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Clone ID: PAT_MRT3847_27747C.1.pep
US-10-424-599-205669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: unsure
LOCATION: (1)..(89)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                          Maxon, Mary
Milne, Todd
No. US20020128250Alman, Thea
Royer, John
Salama, Sofie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-801-368-322
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|1370 IDGTEVDEEFSPEGI 1384
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Best Local Similarity 53.3%;
Matches 8; Conservative
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Best Local Similarity 58.3.
    Cali, Brian
Hecht, Peter
Holtzman, Doug
Madden, Kevin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46 GIKMDDKMPQHG 57
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ORGANISM: Glycine max
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APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Buckharov, Andrey A.
APPLICANT: Buckharov, Andrey A.
APPLICANT: Buckharov, Buckharov, Archive Buckharov, Buckharov, Archive Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckharov, Buckhar
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GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
FILE REFERENCE: 790CTP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT PILLING DATE: 2003-06-11
FRIOR APPLICATION NUMBER: PT/US01/08631
FRIOR FILING DATE: 20001-03-30
FRIOR PILLING DATE: 2000-03-31
FRIOR PILLING DATE: 2000-03-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 45.8%; Score 44; DB 5; Length 159; Best Local Similarity 52.9%; Pred. No. 45; Matches 9; Conservative 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 i LOCATION: (1)._.(159)
i OTHER INFORMATION: Xaa = X or * as defined in Table 2
US-10-450-763-36064
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US-10-437-963-154933
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Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Brazauk, Brad
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US-10-238-075-1472
; Sequence 1472, Application US/10238075
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Best Local Similarity 60.0
Matches 6; Conservative
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ORGANISM: Homo sapiens
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NAME/KEY: misc_feature
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ORGANISM: Oryza sativa
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TITLE OF INVENTION:
TITLE OF INVENTION: E.coli, and biological uses of these polynucleotides and of thei TITLE OF INVENTION: E.coli, and biological uses of these polynucleotides and of thei TITLE OF INVENTION: E.coli, and biological uses of these polynucleotides and of thei TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/10/238,075
CURRENT FILING DATE: 2002-09-10
PRIOR APPLICATION NUMBER: 0003145
PRIOR APPLICATION NUMBER: 0000-03-10
NUMBER OF SEQ ID NOS: 1576
SOFTWARE: Patentin version 3.1
SEQ ID NO 1472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: August 30, 2006, 05:12:59 Job time : 91.9091 secs
Publication No. US20030148324A1 GENERAL INFORMATION:
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58 QKLEDEFPEFTHGLIR 73
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ORGANISM: Escherichia coli
US-10-238-075-1472
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Perfect score:

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Sequence:

Scoring table:

Database

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26724, A
74837, A
167, App
11936, A
893057, A
93092, A
93031, A
89335, A
89335, A
89335, A
89336, A
89336, A
89336, A
89331, A
20831, A
                                                                                         Sequence 167, A Sequence 11936, Sequence 11936, Sequence 99335, Sequence 9335, Sequence 9335, Sequence 20831, Sequence 20831, Sequence 20831, Sequence 30764, Sequence 33843, Sequence 33843, Sequence 33843, Sequence 33843,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR FILING DATE: 2002-05-30
PRIOR FILING DATE: 2002-05-30
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
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Publication No. US20060123505A1
GRNERAL INFORMATION:
APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: National Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-ENGTH PLANT cDNA AND USES THEREOF
FILE REFERENCE: MOA-A020511-US
CURRENT APPLICATION NUMBER: 2001-05-29
PRIOR APPLICATION NUMBER: JP 2002-201369
Sequence
Sequence
Sequence
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                                                          US-11-330-403-7987

US-10-952-500-167

US-10-952-500-167

US-11-056-355B-89336

US-11-056-355B-89335

US-11-056-355B-89335

US-11-056-355B-89334

US-11-056-355B-89334

US-11-056-355B-89334

US-11-056-355B-89334

US-11-056-355B-89334

US-11-056-355B-3059

US-11-056-355B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-3055B-
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US-10-449-902-39837
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Pred. No. 12;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-449-902-33028

'Sequence 33028, Application US/10449902

'Publication No. US20060123505A1

'GENERAL INFORMATION:
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Best Local Similarity ون.٠٠
المحمد وزير Conservative
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282 IEESFPQHGI 291
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US-10-449-902-33028
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LENGTH: 356
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26553, A
68215, A
108651,
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133.695 Million cell updates/sec
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EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
FMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
FMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
FMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
FMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
FMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
FMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
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                                  GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-11-046-35B-6050

US-11-056-35B-6059

US-11-174-307B-286

US-11-174-307B-286

US-11-174-307B-288

US-11-056-35B-6058

US-11-056-35B-109852

US-11-056-35B-119891

US-11-056-35B-119891

US-11-056-35B-119890

US-11-056-35B-119890

US-11-056-35B-119890

US-11-056-35B-119890

US-11-056-35B-119890

US-11-056-35B-119890

US-11-056-35B-119890

US-11-056-35B-119890

US-11-056-35B-119890

US-11-056-35B-119890

US-11-056-35B-68214

US-11-174-3018-2110

US-11-174-3018-2110

US-11-056-35B-119889

US-11-056-35B-119889

US-11-056-35B-119889

US-11-056-35B-119889
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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96
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Maximum DB seq length: 200000000
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6 VDEQFPQHGL 15
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; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR PLING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NOS: 119966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: BLOVEL, Vyduneslav
APPLICANT: Alexandrov, Nickolai
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
TITLE OF INVENTION: Polypeptides Encoded Thereby
TITLE OF INVENTION: Polypeptides Encoded Thereby
TITLE OF INVENTION: 2019-19082
CURRENT APPLICATION NUMBER: 05/11/056,355B
CURRENT FILING DATE: 2005-02-14
PRIOR PAPLICATION NUMBER: 60/544,190
PRIOR APPLICATION NUMBER: 60/544,190
NUMBER OF SEQ ID NOS: 119966
SEQ ID NO 6060
LENGTH: 321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; NAME/KEY: peptide
; LOCATION: (1)..(321)
; OTHER INDEMATION: Ceres Seq. ID no. 12344159
US-11-056-355B-6060
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SCPTWARE: Patentin Ver. 2.1
SEQ ID NO 47548
LENGTH: 376
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; Publication No. US20060150283A1
; GENERAL INFORMATION:
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ORGANISM: Zea mays subsp. mays
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ORGANISM: Zea mays subsp. mays
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Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 70.0
Matches 7; Conservative
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246 VEEGFPQHGI 255
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US-10-449-902-47548
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US-11-056-355B-6059
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LOCATION:
OTHER INFORMATION: GI Number: 3851003; NR Description: pyruvate dehydrogenase
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OTHER INFORMATION: GI Number: 3851001; NR Description: pyruvate dehydrogenase
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OTHER INFORMATION: GI Number: 520478; NR Description: pyruvate dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: ALEXANDROV, Nickolai
APPLICANT: ALEXANDROV, Nickolai
APPLICANT: BROVER, Vyacheelav
ITITE OP INVENTION: UVCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY
ITITE OP INVENTION: USEFUL FOR MODIFYING PLANT CHARACTERISTICS
CURRENT APPLICATION NUMBER: US/11/174,307B
CURRENT FILING DATE: 2005-06-30
PRIOR APPLICATION NUMBER: 60/583,671
PRIOR APPLICATION NUMBER: 60/583,671
PRIOR APPLICATION NUMBER: 60/583,651
PRIOR PILING DATE: 2004-06-30
PRIOR PILING DATE: 2004-06-30
PRIOR PILING DATE: 2004-06-30
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US-11-174-307B-286
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NAME/KEY: peptide
LOCATION: (1)..(373)
OTHER INFORMATION: Ceres Seq. ID no. 12344158
                                                                                                                                                                                                                       44.8%; Score 43; DB 70.0%; Pred. No. 18; iive 2; Mismatches
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Best Local Similarity 70.0
Matches 7; Conservative
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NAME/KEY: misc_feature
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Sequence 30777, Application US/10449902

Bublication No. US20060123505A1

GENERAL INFORMATION:
GENERAL INFORMATION:
HOPPICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
TITLE OF INVENTION: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
FILE REFERENCE: MOA-A020571-US
CURRENT PILING DATE: 2003-05-39
PRIOR FILING DATE: 2003-05-30
PRIOR FILING DATE: 2002-05-30
PRIOR FILING DATE: 2002-05-30
PRIOR FILING DATE: 2002-012-11
NUMBER OF SEQ ID NOS: 56791

SOFTWARE: PatentIN Ver. 2.1

LENGTH: 273
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding FITLE OF INVENTION: Polypeptides Encoded Thereby FILE 2750-1590FUGS ENCORENT TRING DATE: 2705-0-1590FUGS ENCORENT FILING DATE: 2005-02-14 PRIOR APPLICATION NUMBER: 60/544,190 PRIOR FILING DATE: 2004-02-13 PRIOR FILING DATE: 2004-02-13 ENGRED FILING DATE: 2004-02-13 ENGRED FILING DATE: 2004-02-13 ENGRED FILING DATE: 2004-02-13 ENGRED FILING DATE: 2004-02-13 ENGRED FILING DATE: 2004-02-13 ENGRED FILING DATE: 2004-02-13 ENGRED FILING DATE: 2004-02-13 ENGRED FILING DATE: 2004-02-13 ENGRED FILING DATE: 2004-02-13 ENGRED FILING DATE: 2004-02-13 ENGRED FILING DATE: 2004-02-13 ENGRED FILING DATE: 2004-02-13 ENGRED FILING DATE: 2004-02-13 ENGRED FILING DATE: 2004-02-13 ENGRED FILING DATE: 2004-02-13 ENGRED FILING DATE: 2004-02-13 ENGRED FILING DATE: 2004-02-13 ENGRED FILING DATE: 2004-02-13 ENGRED FILING DATE: 2004-02-13 ENGRED FILING DATE: 2004-02-13 ENGRED FILING DATE: 2004-02-13 ENGRED FILING DATE: 2004-02-13 ENGRED FILING DATE: 2004-02-13 ENGRED FILING DATE: 2004-02-13 ENGRED FILING DATE: 2004-02-13 ENGRED FILING DATE: 2004-02-13 ENGRED FILING DATE: 2004-02-13 ENGRED FILING DATE: 2004-02-13 ENGRED FILING DATE: 2004-02-13 ENGRED FILING DATE: 2004-02-13 ENGRED FILING DATE: 2004-02-13 ENGRED FILING DATE: 2004-02-13 ENGRED FILING DATE: 2004-02-13 ENGRED FILING DATE: 2004-02-13 ENGRED FILING DATE: 2004-02-13 ENGRED FILING DATE: 2004-02-13 ENGRED FILING DATE: 2004-02-13 ENGRED FILING DATE: 2004-02-13 ENGRED FILING DATE: 2004-02-13 ENGRED FILING FILING DATE: 2004-02-13 ENGRED FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FILING FI
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Publication No. US20060150283A1
GENERAL INFORMATION:
APPLICANT: Brover, Vyacheslav
APPLICANT: Alexandrov, Nickolai
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENCE: 2750-1590PUS2
CURRENT APPLICATION NUMBER: US/11/056,355B
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Pred. No. 22;
2; Mismatches
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Pred. No. 19;
2; Mismatches
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OTHER INFORMATION: Ceres Seq. ID no. 12344157
                                                                                                                                                                                                                                                                                                                                                                           TYPE: prt
ORGANISM: Zea mays subsp. mays
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Best Local Similarity 63.00
Best Local 7; Conservative
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Best Local Similarity 70.0
Matches 7; Conservative
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373 VEEGFPOHGI 382
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US-10-449-902-30777
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US-11-056-355B-26554
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OTHER INFORMATION: GI Number: 3851003; NR Description: pyruvate dehydrogenase El
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; OTHER INFORMATION: GI Number: 25012844; NR Description: RH05604p [Drosophila
US-11-174-307B-288
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CURRENT APPLICATION NUMBER: US/11/174,307B
CURRENT FILING DATE: 2005-06-30
PRIOR FILING DATE: 2004-06-30
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Pred. No. 20;
2; Mismatches 1; Indels
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; Sequence 6058, Application US/11056355B

; Publication No. US20060150283A1

; GENERAL INFORMATION:
                                                                                                                                                                                                                      Sequence 288, Application US/11174307B
Publication No. US20060143729A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai
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Best Local Similarity 70.0
300 VEEGFPOHGI 309
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NAME/KEY: misc_feature
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ORGANISM: Zea mays
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TYPE: prt
ORGANISM: Arabidopsis thaliana
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; ORGANISM: Triticum aestivum
US-10-953-349-26705
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Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                    Query Match
Best Local Similarity 70.0°
Matches 7; Conservative
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Best Local Similarity 70.0
Matches 7; Conservative
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260 VEEGFPQHGV 269
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246 VEEGFPQHGV 255
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                                                                                                                                                                                                                                                                                                                                                          US-10-953-349-26705
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Sequence 119891, Application US/11056355B

Sequence 119891, Application No. US20060150283A1

GENERAL INFORMATION:
APPLICANT: Brover, Vyacheslav
APPLICANT: Brover, Vyacheslav
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENCE: 275-159PUS2

CURRENT APPLICATION NUMBER: US/11/056,355B

CURRENT APPLICATION NUMBER: 05/544,190

PRIOR APPLICATION NUMBER: 60/544,190

PRIOR FILING DATE: 2004-02-13

NUMBER OF SEQ ID NOS: 119966

SEQ ID NO 119891
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US-11-056-355B-108652

Sequence 108652, Application US/11056355B

Publication No. US2066150283A1

GENERAL INFORMATION:
APPLICANT: Brover, Vyacheslav

APPLICANT: Alexandrov, Nickolai
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENCE: 2750-1590PUS2

CURRENT APPLICATION NUMBER: US/11/056,355B

CURRENT FILING DATE: 2005-02-14

PRIOR PILING DATE: 2004-02-13

NUMBER OF SEQ ID NOS: 119966

SEQ ID NO 108652
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Pred. No. 22;
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Pred. No. 22;
2; Mismatches 1; Indels
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; OTHER INFORMATION: Ceres Seq. ID no. 12384700
US-11-056-355B-26554
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; OTHER INFORMATION: Ceres Seq. ID no. 13668006
US-11-056-355B-108652
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PRIOR APPLICATION NUMBER: 60/544,190 PRIOR FILING DATE: 2004-02-13 NUMBER OF SEQ ID NOS: 119966 SEQ ID NO 26554 LENGTH: 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: prt
ORGANISM: Arabidopsis thaliana
                                                                                                   TYPE: prt
ORGANISM: Arabidopsis thaliana
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Best Local Similarity 70.0%;
Matches 7; Conservative
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246 VEEGFPQHGV 255
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                                                                                                                                                          NAME/KEY: peptide
LOCATION: (1)..(3)
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Sequence 26705, Application US/10953349
Sequence 26705, Application No. US20060107345A1
GENERAL INFORMATION:
TELL INFORMATION:
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
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; Sequence 26553, Application WS/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
    APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; TITLE OF INVENTION: VMPBER: US/11/056,355B
; CURRENT APPLICATION NUMBER: 60/544,190
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR APPLICATION NUMBER: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 26553
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                                                                                                                                                                                        Length 314;
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70.0%; Pred. No. 23;
tive 2; Mismatches
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(314)
; OTHER INFORMATION: Ceres Seq. ID no. 13668006
US-11-056-355B-119891
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; OTHER INFORMATION: Ceres Seq. ID no. 12384699
US-11-056-355B-26553
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                                                                                                                                                                                        Score 42; DB 7 Pred. No. 22; 2; Mismatches
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Publication No. US20060150283A1

GENERAL INCORMATION:

APPLICANT: Brover, Vyacheslav

APPLICANT: Alexandrov, Nickolai

TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding

TITLE OF INVENTION: Polypptides Encoded Thereby

FILE REFERENCE: 2750-1590FUS2

CURRENT FILING DATE: 2005-02-14

PRIOR APPLICATION NUMBER: US/11/056,355B

CURRENT FILING DATE: 2004-02-13

PRIOR PRIOR PILING DATE: 2004-02-14

PRIOR PRIOR OF SEQ ID NOS: 119966

SEQ ID NO 108651
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                                                                                                      RESULT 14
US-11-056-355B-68215
; Sequence 68215, Application US/11056355B
; Publication No. US20060150283A1
; GENREAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REPERRENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR PELING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 68215
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43.8%; Score 42; DB 7; Length 328;
Best Local Similarity 70.0%; Pred. No. 23;
Matches 7; Conservative 2; Mismatches 1; Indels
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    NAME/KEY: peptide
    LOCATION: (1) . (328)
    OTHER INFORMATION: Ceres Seq. ID no. 13596007
    USE-11-056-355B-68215
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; LOCATION: (1)..(328)
; OTHER INFORMATION: Ceres Seq. ID no. 13668005
US-11-056-355B-108651
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ORGANISM: Arabidopsis thaliana
FEATURE:
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ORGANISM: Triticum aestivum
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260 VEEGFPQHGV 269
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260 VEEGFPQHGV 269
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260 VEEGFPQHGV 269
6 VDEOFPOHGL 15
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